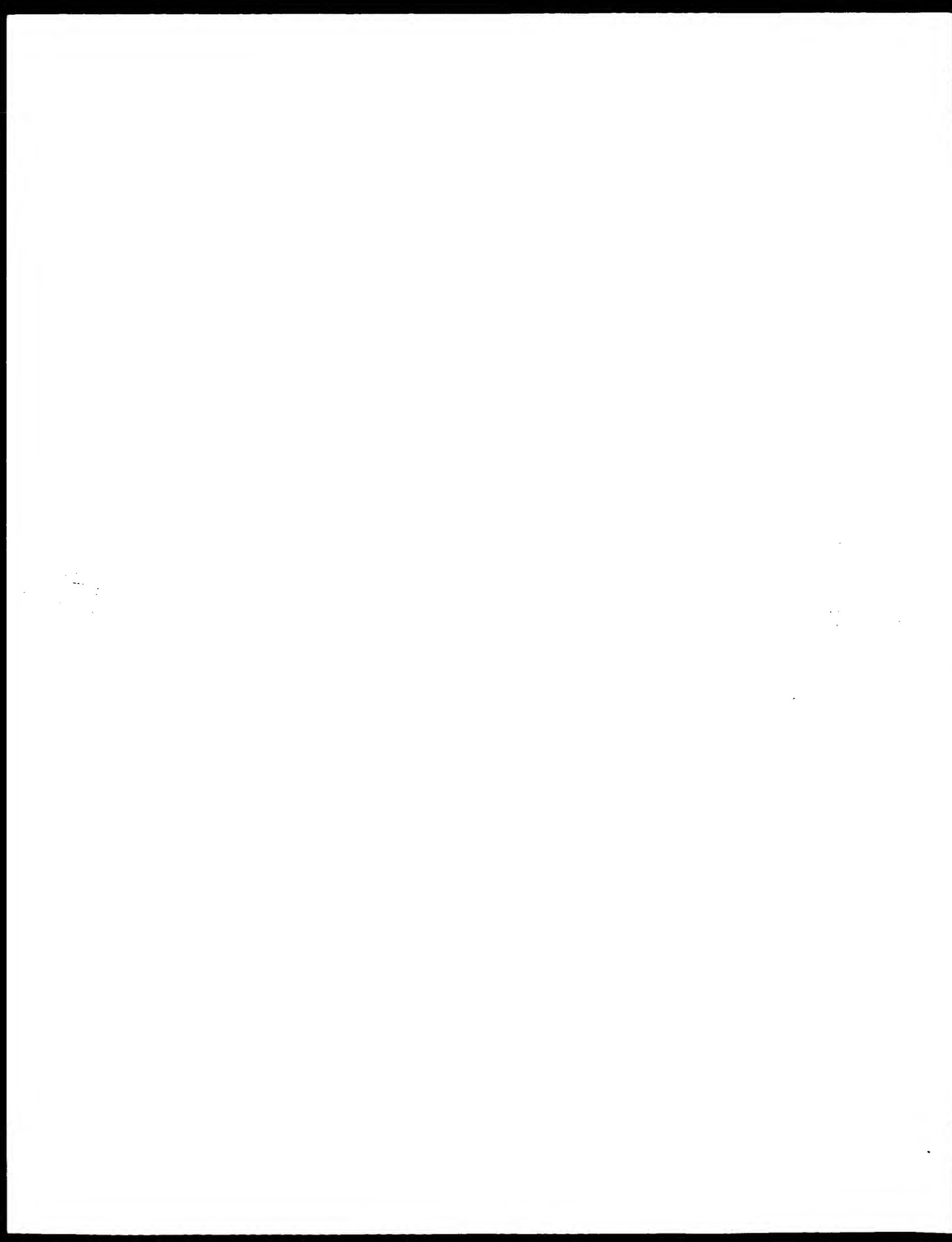


XX 27 AUG-1998.
 XX 19-FEB-1998; 98WO-USO3041.
 XX 20-FEB-1997; 97US-0038118.
 XX (BAYH) BAYLOR COLLEGE MEDICINE.
 XX (TEXA) UNIV TEXAS SYSTEM.
 XX Benedict WF, Hu S, Xu H, Zhou Y;
 XX WFT: 1998-480788/41.
 XX P PSUB; AAW69367.
 XX Retinoblastoma suppressor protein with N terminal modification -
 XX inhibiting cellular proliferation, particularly cancer
 XX Claim 22; File 159 162; 249pp, English.
 XX This sequence encodes a modified retinoblastoma tumour suppressor
 XX protein (RbSp) of the invention. The proteins can be used for inhibiting
 XX cellular proliferation, when coadministered with a p53 protein. The RbSpS
 XX can be used for treating diseases characterised by abnormal cellular
 XX proliferation, particularly cancers. The RbSpS have a broader spectrum of
 XX activity than wild type RbSpS.
 XX Sequence 3323 BP; 1114 A; 605 C; 591 G; 1013 T; 0 other;
 XX
 XX Query Match 95.9%; Score 3315; DB 19; Length 3323;
 XX Best Local Similarity 100.0%; Fwd N-G.
 XX Matches 3315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 XX 141 GGACAAACCTTCACATCTCCATGACATATGGCAGGCTTATATTCAAAAGAAAAAGCACT 200
 XX 9 GAAAGAAATTTCTATCATGATGATGATTTGGGAGCTTATATTCAAAAGAAAAAGCACT 68
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 XX 201 GTGGGAAATCTATCTTTATTCAGAGATGATGATGATGATGATGATGATGATGATGAT 260
 XX 49 GTGGGAAATCTATCTTTATTCAGAGATGATGATGATGATGATGATGATGATGATGAT 128
 XX 161 TGAGATACAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 320
 XX 129 TGAGATACAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 188
 XX 321 TGAGATACAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 380
 XX 189 TGAGATACAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 248
 XX 381 GTGGGAAATCTATCTTTATTCAGAGATGATGATGATGATGATGATGATGATGATGAT 440
 XX 249 GTGGGAAATCTATCTTTATTCAGAGATGATGATGATGATGATGATGATGATGATGAT 308
 XX 441 TGAGATACAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 500
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 XX 469 TGAGATACAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 428
 XX 561 TGAGATACAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 620
 XX 429 TGAGATACAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 488
 XX 621 TGAGATACAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 680
 XX 489 TGAGATACAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 548
 XX 681 TGAGATACAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 740
 XX 549 TGAGATACAGAAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 608

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January 16, 2003, 15:20:22 : Search time 59.681 seconds
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us-09-026-459a-42

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Gapop 10.0 : Gapext 1.0

Searches: 441962 seqs, 15336881 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post processing: Minimum Match 9%
Maximum Match 100%
Listing first 45 summaries

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- 1: Zom2 6/9/94/4712/17A Comp seq *
- 2: Zom2 6/9/94/4712/17B Comp seq *
- 3: Zom2 6/9/94/4712/17C Comp seq *
- 4: Zom2 6/9/94/4712/17D Comp seq *
- 5: Zom2 6/9/94/4712/17E Comp seq *
- 6: Zom2 6/9/94/4712/17F Comp seq *

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4004.4	89.8	3242	1	US-08-048-760-1 Sequence 1, Appl
2	4004.4	89.8	3242	1	US-08-048-760-2 Sequence 2, Appl
3	4004.4	89.8	3242	1	US-08-470-091-1 Sequence 1, Appl
4	4004.4	89.8	3242	2	US-08-470-091-2 Sequence 2, Appl
5	2433.6	72.7	2994	1	US-08-294-329-2 Sequence 2, Appl
6	2433.6	72.7	2994	3	US-08-851-092-3 Sequence 3, Appl
7	2433.6	72.7	2994	4	US-09-415-113-3 Sequence 3, Appl
8	2432.2	72.7	2994	2	US-08-482-627-4 Sequence 4, Appl
9	2430.8	72.6	2995	2	US-08-959-638-7 Sequence 7, Appl
10	2429.6	72.6	2994	5	PT-0394-10357-1 Sequence 1, Appl
11	2429.2	72.6	2994	4	US-08-339-674A-7 Sequence 7, Appl
12	68.8	2.1	2808	1	US-07-708-962-1 Sequence 1, Appl
13	68.2	2.0	3249	1	US-08-106-493A-1 Sequence 1, Appl
14	68.2	2.0	3249	1	US-08-429-254-1 Sequence 1, Appl
15	68.2	2.0	4853	1	US-08-852-883-1 Sequence 1, Appl
16	68.2	2.0	4853	2	US-08-852-877-1 Sequence 1, Appl
17	65.6	4.9	2808	2	US-08-152-7218-1 Sequence 1, Appl
18	59	1.8	7238	1	US-08-212-453-14 Sequence 14, Appl
19	51	1.5	3747	4	US-09-237-2935-2 Sequence 2, Appl
20	44.6	1.3	1803	4	US-09-144-001C-796 Sequence 799, App
21	44.6	1.3	15463	4	US-08-961-527-139 Sequence 139, App
22	44.4	1.3	20674	4	US-09-641-638-651 Sequence 651, App
23	44	1.3	19124	2	US-08-487-8268-13 Sequence 13, Appl
24	43.8	1.3	1056	4	US-09-134-001C-1550 Sequence 1550, App
25	43.2	1.3	509	4	US-09-609-607-202 Sequence 202, App
26	43.2	1.3	509	4	US-09-609-785-292 Sequence 292, App
27	43.2	1.3	509	4	US-09-439-313-292 Sequence 292, App

28	43.2	1.3	509	4	US-09-352-614A-202 Sequence 202, App
29	43.2	1.3	509	4	US-09-352-614A-202 Sequence 202, App
30	43	1.3	5852	1	US-07-867-106-292 Sequence 2, Appl
31	42.8	1.3	615	4	US-08-998-416-186 Sequence 186, App
32	42.6	1.3	1189	1	US-08-407-591-2 Sequence 2, Appl
33	42.6	1.3	2654	4	US-09-234-827B-3 Sequence 3, Appl
34	42.4	1.3	1186	2	US-08-731-722-5 Sequence 5, Appl
35	42.4	1.3	1774	1	US-08-742-001-29 Sequence 29, Appl
36	42	1.3	665	2	US-08-883-795A-36 Sequence 46, Appl
37	42	1.3	1864	4	US-09-468-265-4 Sequence 4, Appl
38	41.8	1.2	1670	4	US-09-306-060-1 Sequence 1, Appl
39	41.4	1.2	15124	2	US-08-487-826B-14 Sequence 14, Appl
40	41.2	1.2	821	4	US-08-998-416-541 Sequence 541, App
41	41.2	1.2	837	4	US-08-998-416-288 Sequence 288, App
42	41.2	1.2	2030	2	US-08-705-537-7 Sequence 7, Appl
43	40.8	1.2	1144	1	US-08-014-944A-1 Sequence 1, Appl
44	40.8	1.2	1144	1	US-08-486-421-2 Sequence 2, Appl
45	40.8	1.2	1144	1	US-08-470-911-2 Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-048-760-1
Sequence 1, Application US/08038760
Patent No. 5496731
GENERAL INFORMATION:
APPLICANT: Xu, Hong-Ji
APPLICANT: Bu, Shi-Xue
TITLE OF INVENTION: Broad spectrum tumor suppressor genes, gene products and methods for their use
INVENTOR: Xu, Hong-Ji
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ponsio & Edwards
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/048,760
FILING DATE: 1999.04.25
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ponsio & Edwards
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7499 025 909
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 750-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3232 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 19...2469
US-08-048-760-1

Query Match: 89.8%, Score: 4004.4, DB 1, Length: 3242;
Best Local Similarity: 100.0%, Prod. No. 0;
Matches: 3605, Conservative: 0, Mismatches: 1, Indels: 0, Gaps: 0;

[illegible]

1 NUMBER OF SEQUENCES: 4
 2 CORRESPONDENCE ADDRESS:
 3 ADDRESSEE: Temple University of the Commonwealth
 4 ADDRESSEE: System of Higher Education
 5 STREET: 406 University Services Building
 6 CITY: Philadelphia
 7 STATE: Pennsylvania
 8 COUNTRY: U.S.A.
 9 ZIP: 19122
 10 COMPUTER READABLE FORM:
 11 MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
 12 COMPUTER: IBM PS/2
 13 OPERATING SYSTEM: MS DOS
 14 SOFTWARE: WordPerfect 5.1
 15 CURRENT APPLICATION DATA:
 16 APPLICATION NUMBER: US 09/016 494
 17 FILING DATE: August 12, 1994
 18 CLASSIFICATION: 4.50
 19 PRIOR APPLICATION DATA:
 20 APPLICATION NUMBER:
 21 FILING DATE:
 22 ATTORNEY/AGENT INFORMATION:
 23 NAME: Mullins, J.G.
 24 REGISTRATION NUMBER: 35,074
 25 REFERENCE/DOCKET NUMBER: 6056-188
 26 TELECOMMUNICATION INFORMATION:
 27 TELEPHONE: (215) 568-8484
 28 TELEFAX: (215) 568-5549
 29 TELE: No. 545/0490
 30 INFORMATION FOR SEQ ID NO: 1:
 31 SEQUENCE CHARACTERISTICS:
 32 LENGTH: 4249 base pairs
 33 TYPE: nucleic acid
 34 STRANDEDNESS: Single
 35 TOPOLOGY: Linear
 36 US 09 106 494A 1

Query Match 2.08; Score 68.2; Db 1; Length 4249;
 Best Local Similarity 53.09; Pred. No. 1.0e-07;
 Matches 170; Conservative 0; Mismatches 148; Indels 3; Gaps 1.

QY 1715 AGAAGCATTGAAATGATCTTTTCACTGTTTATATAAAAGATGATGGCTAGGCT 1774
 DB 2312 ATAGAGGAG 2371
 QY 1775 AATGCTGGCTAAATACATCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAG 1834
 DB 2372 ATAG 2428
 QY 1835 TATCTGAG 1894
 DB 2429 AATGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 2488
 QY 1895 AATGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 1954
 DB 2489 AATGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 2548
 QY 1955 TAAATGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 2014
 DB 2549 AATGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 2608
 QY 2015 TCAAG 2075
 DB 2609 ATAG 2629

RESULT 14
 US-08-429-264-1
 Sequence 1, Application US/0942654
 Patent No. 554240
 GENERAL INFORMATION:
 APPLICANT: Antonio Giordano
 TITLE OF INVENTION: *TUMOR SUPPRESSOR PROTEIN

1 TITLE OF INVENTION: PRB2*
 2 NUMBER OF SEQUENCES: 4
 3 CORRESPONDENCE ADDRESS:
 4 ADDRESSEE: Seidel, Gonda, Lavorata & Monaco, P.C.
 5 STREET: 1800 Two Penn Center Plaza
 6 CITY: Philadelphia
 7 STATE: Pennsylvania
 8 COUNTRY: U.S.A.
 9 ZIP: 19102
 10 COMPUTER READABLE FORM:
 11 MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
 12 COMPUTER: IBM PS/2
 13 OPERATING SYSTEM: MS-DOS
 14 SOFTWARE: WordPerfect 5.1
 15 CURRENT APPLICATION DATA:
 16 APPLICATION NUMBER: 09/016,494
 17 FILING DATE: August 12, 1994
 18 CLASSIFICATION: 5.50
 19 PRIOR APPLICATION DATA:
 20 APPLICATION NUMBER: 08/106,494
 21 FILING DATE: August 12, 1994
 22 ATTORNEY/AGENT INFORMATION:
 23 NAME: Monaco, D.A.
 24 REGISTRATION NUMBER: 40,480
 25 REFERENCE/DOCKET NUMBER: 6056-188 D11
 26 TELECOMMUNICATION INFORMATION:
 27 TELEPHONE: (215) 568-8484
 28 TELEFAX: (215) 568-5549
 29 TELE: No. 55323400
 30 INFORMATION FOR SEQ ID NO: 1:
 31 SEQUENCE CHARACTERISTICS:
 32 LENGTH: 4249 base pairs
 33 TYPE: nucleic acid
 34 STRANDEDNESS: Single
 35 TOPOLOGY: Linear
 36 US-08-429-264-1

Query Match 2.08; Score 68.2; Db 1; Length 4249;
 Best Local Similarity 53.09; Pred. No. 1.0e-07;
 Matches 170; Conservative 0; Mismatches 148; Indels 3; Gaps 1.

QY 1715 AGAAGCATTGAAATGATCTTTTCACTGTTTATATAAAAGATGATGGCTAGGCT 1774
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 QY 1835 TATCTGAG 1894
 DB 2429 AATGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 2488
 QY 1895 AATGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 1954
 DB 2489 AATGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCTGGCT 2548
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 QY 2015 TCAAG 2075
 DB 2609 ATAG 2629

RESULT 15
 US-08-429-264-1
 Sequence 1, Application US/0942654
 Patent No. 5807681
 GENERAL INFORMATION:
 APPLICANT: Giordano, Antonio
 APPLICANT: Baldi, Alphonso

TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS AND PROGNOSIS
TITLE OF INVENTION: OF CANCER

2. I have been advised that the following information is being furnished to the FBI:

CORRESPONDENCE ADDRESS:

ADDRESSER: SEIDEL, GÜNDA, LAVORGNA & MONACO, P.C.

STREET: Suite 1800 Two Penn Center Plaza

City: Philadelphia

STATE: PA

• NILEY: USA

200: 19102

CONCLUSIONS AND RECOMMENDATIONS

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

Source: FIWARE: Patent In Release #1.0, Version #1.30

CHRYSLER APPL [CALLION DATA:

APPLICATION NUMBER: US/08/932,883

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: MONACO, Daniel A

REF: SIRAJI UN NUMBER: 30,480

REFERENCE/INDEX NUMBER: 8321-13 US1

ELECTRONIC COMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8383

TELEFAX: (215) 568-5549

THE MAXIMUM OF $\sum_{i=1}^n x_i$ IS 1.

SCIENCE CHARACTERISTICS

UNITED STATES PATENT OFFICE

TYPE: carboxylic acid

TYPE: MINERAL: double
STRAUNFELD: double

T. POLINSKY, LINDA R. KATZMELDNER, (M)

THE UNIVERSITY OF CHICAGO

W. J. R. 1971.

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NAME/REF.	CDS
W. B. R. T. N.	70
W. B. R. T. N.	70

1. 2. 3. 4. 5. 6. 7. 8. 9. 10. 11. 12. 13. 14. 15. 16. 17. 18. 19. 20. 21. 22. 23. 24. 25. 26. 27. 28. 29. 30. 31. 32. 33. 34. 35. 36. 37. 38. 39. 40. 41. 42. 43. 44. 45. 46. 47. 48. 49. 50. 51. 52. 53. 54. 55. 56. 57. 58. 59. 60. 61. 62. 63. 64. 65. 66. 67. 68. 69. 70. 71. 72. 73. 74. 75. 76. 77. 78. 79. 80. 81. 82. 83. 84. 85. 86. 87. 88. 89. 90. 91. 92. 93. 94. 95. 96. 97. 98. 99. 100. 101. 102. 103. 104. 105. 106. 107. 108. 109. 110. 111. 112. 113. 114. 115. 116. 117. 118. 119. 120. 121. 122. 123. 124. 125. 126. 127. 128. 129. 130. 131. 132. 133. 134. 135. 136. 137. 138. 139. 140. 141. 142. 143. 144. 145. 146. 147. 148. 149. 150. 151. 152. 153. 154. 155. 156. 157. 158. 159. 160. 161. 162. 163. 164. 165. 166. 167. 168. 169. 170. 171. 172. 173. 174. 175. 176. 177. 178. 179. 180. 181. 182. 183. 184. 185. 186. 187. 188. 189. 190. 191. 192. 193. 194. 195. 196. 197. 198. 199. 200. 201. 202. 203. 204. 205. 206. 207. 208. 209. 210. 211. 212. 213. 214. 215. 216. 217. 218. 219. 220. 221. 222. 223. 224. 225. 226. 227. 228. 229. 230. 231. 232. 233. 234. 235. 236. 237. 238. 239. 240. 241. 242. 243. 244. 245. 246. 247. 248. 249. 250. 251. 252. 253. 254. 255. 256. 257. 258. 259. 260. 261. 262. 263. 264. 265. 266. 267. 268. 269. 270. 271. 272. 273. 274. 275. 276. 277. 278. 279. 280. 281. 282. 283. 284. 285. 286. 287. 288. 289. 290. 291. 292. 293. 294. 295. 296. 297. 298. 299. 300. 301. 302. 303. 304. 305. 306. 307. 308. 309. 310. 311. 312. 313. 314. 315. 316. 317. 318. 319. 320. 321. 322. 323. 324. 325. 326. 327. 328. 329. 330. 331. 332. 333. 334. 335. 336. 337. 338. 339. 340. 341. 342. 343. 344. 345. 346. 347. 348. 349. 350. 351. 352. 353. 354. 355. 356. 357. 358. 359. 360. 361. 362. 363. 364. 365. 366. 367. 368. 369. 370. 371. 372. 373. 374. 375. 376. 377. 378. 379. 380. 381. 382. 383. 384. 385. 386. 387. 388. 389. 390. 391. 392. 393. 394. 395. 396. 397. 398. 399. 400. 401. 402. 403. 404. 405. 406. 407. 408. 409. 410. 411. 412. 413. 414. 415. 416. 417. 418. 419. 420. 421. 422. 423. 424. 425. 426. 427. 428. 429. 430. 431. 432. 433. 434. 435. 436. 437. 438. 439. 440. 441. 442. 443. 444. 445. 446. 447. 448. 449. 450. 451. 452. 453. 454. 455. 456. 457. 458. 459. 460. 461. 462. 463. 464. 465. 466. 467. 468. 469. 470. 471. 472. 473. 474. 475. 476. 477. 478. 479. 480. 481. 482. 483. 484. 485. 486. 487. 488. 489. 490. 491. 492. 493. 494. 495. 496. 497. 498. 499. 500. 501. 502. 503. 504. 505. 506. 507. 508. 509. 510. 511. 512. 513. 514. 515. 516. 517. 518. 519. 520. 521. 522. 523. 524. 525. 526. 527. 528. 529. 530. 531. 532. 533. 534. 535. 536. 537. 538. 539. 540. 541. 542. 543. 544. 545. 546. 547. 548. 549. 550. 551. 552. 553. 554. 555. 556. 557. 558. 559. 560. 561. 562. 563. 564. 565. 566. 567. 568. 569. 570. 571. 572. 573. 574. 575. 576. 577. 578. 579. 580. 581. 582. 583. 584. 585. 586. 587. 588. 589. 590. 591. 592. 593. 594. 595. 596. 597. 598. 599. 600. 601. 602. 603. 604. 605. 606. 607. 608. 609. 610. 611. 612. 613. 614. 615. 616. 617. 618. 619. 620. 621. 622. 623. 624. 625. 626. 627. 628. 629. 630. 631. 632. 633. 634. 635. 636. 637. 638. 639. 640. 641. 642. 643. 644. 645. 646. 647. 648. 649. 650. 651. 652. 653. 654. 655. 656. 657. 658. 659. 660. 661. 662. 663. 664. 665. 666. 667. 668. 669. 670. 671. 672. 673. 674. 675. 676. 677. 678. 679. 680. 681. 682. 683. 684. 685. 686. 687. 688. 689. 690. 691. 692. 693. 694. 695. 696. 697. 698. 699. 700. 701. 702. 703. 704. 705. 706. 707. 708. 709. 710. 711. 712. 713. 714. 715. 716. 717. 718. 719. 720. 721. 722. 723. 724. 725. 726. 727. 728. 729. 730. 731. 732. 733. 734. 735. 736. 737. 738. 739. 740. 741. 742. 743. 744. 745. 746. 747. 748. 749. 750. 751. 752. 753. 754. 755. 756. 757. 758. 759. 760. 761. 762. 763. 764. 765. 766. 767. 768. 769. 770. 771. 772. 773. 774. 775. 776. 777. 778. 779. 780. 781. 782. 783. 784. 785. 786. 787. 788. 789. 790. 791. 792. 793. 794. 795. 796. 797. 798. 799. 800. 801. 802. 803. 804. 805. 806. 807. 808. 809. 810. 811. 812. 813. 814. 815. 816. 817. 818. 819. 820. 821. 822. 823. 824. 825. 826. 827. 828. 829. 830. 831. 832. 833. 834. 835. 836. 837. 838. 839. 840. 84

Mathias

2.06; SEC: 38.2; DB: 1; Length: 4853;
53.08; DB: 1; 90-07.

Model similarity: 33.0%; Pred. NO: 1.9E-07;
 AUCs: 170: Conservat (w) 0; Mismatches 148

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RESULT 4

US-09-315-1113-3

Sequence 3, Application US/09315113

Patent No. 6379927

GENERAL INFORMATION:

APPLICANT: Antelman, Douglas

Gregory, Richard J.

Wills, Kenneth N.

TITLE OF INVENTION: Tissue Specific Expression of

Retinoblastoma Protein

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP

STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-Les/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/315,113

FILING DATE: 10-May-1999

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/801,092

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

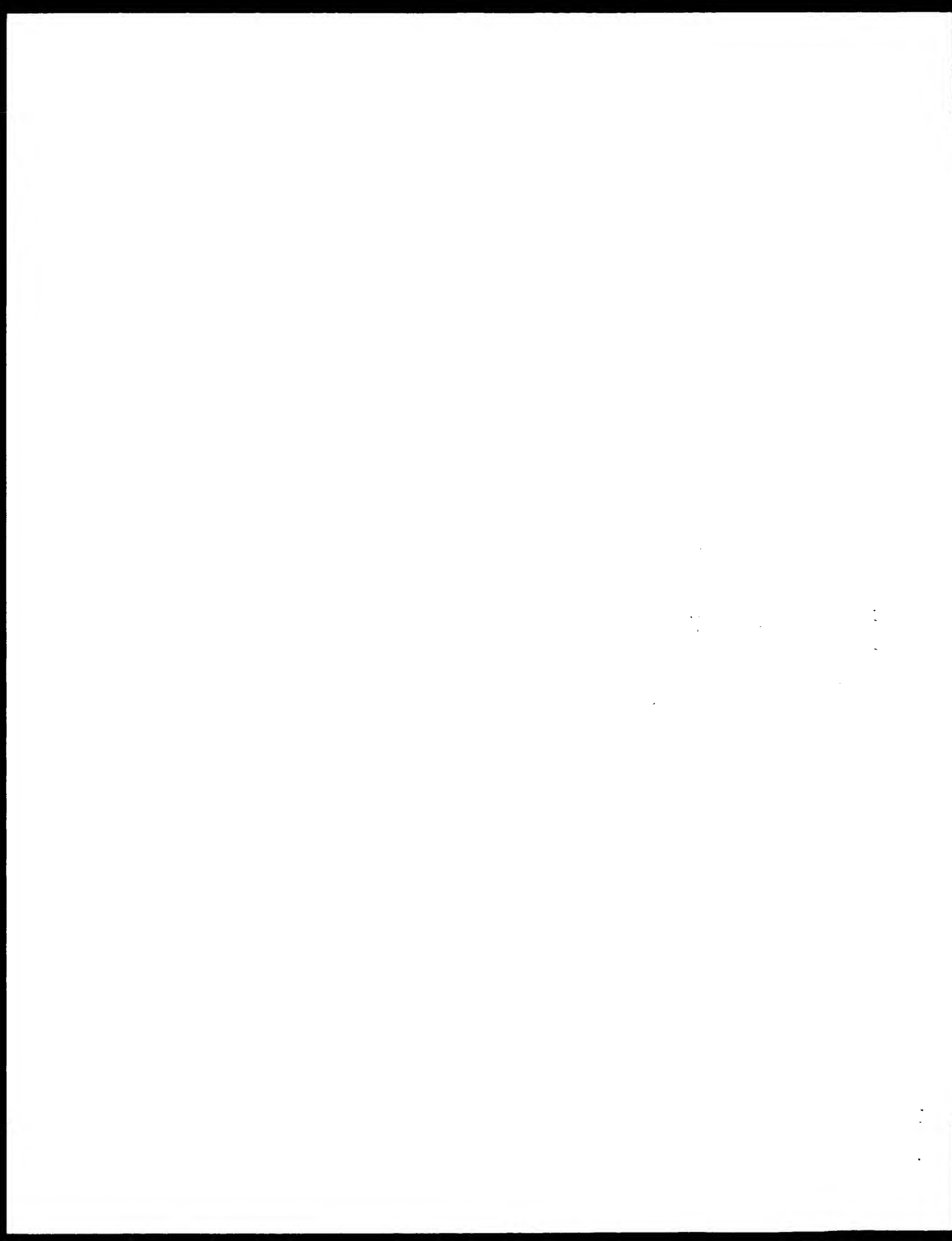
NAME: Ellis, Renee A.

REGISTRATION NUMBER: 35,136

[illegible]

RESULT 11
 1. TITLE OF INVENTION: 591-2/c
 2. SUBSEQUENT 2. Application US/084700941
 3. PRIORITY NO. 5912246
 4. GENERAL INFORMATION:
 5. APPLICANT: XU, HONG-JI
 6. APPLICANT: HU, SHI XUE
 7. APPLICANT: BENEDICT, WILLIAM F.
 8. TITLE OF INVENTION: BROAD SPECTRUM Tumor Suppressor Genes, Gene Products and
 9. TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.

| | | | |
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| Alignment Scores: | 0 | Length: | 3232 |
| Pred. No.: | 0 | | |



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561 LeuAlaIleProLeuSerProGluPheAspLeuIleTyrGlnSerLysAspArgLeu 580
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1949 ATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1998
621 ArgValAspSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLys 640
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2119 GAT 2178
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QY 921 AspThrSerAsnLysGlnLysLys 928
Db 2899 GATACCTCAAAACAGAAAGAGAAA 2922
RESULT 8
US-08-038-760-1
Sequence 1, Application US/08048760
Patent No. 5496731
GENERAL INFORMATION:
APPLICANT: Xu, Hong-li
APPLICANT: Hu, Shi Xue
APPLICANT: Benedict, William F.
TITLE OF INVENTION: Broad Spectrum Tumor Suppressor Genes, Gene Products and
TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Poulie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10046-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/048,760
FILING DATE: 19930325
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Polissant, Brian M
REGISTRATION NUMBER: 28,462
REFERENCE/DOCKET NUMBER: 7409-025-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790,9090
TELEFAX: (212) 869,9741/8864
TELEX: 64141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3232 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 19..2469
US-08-038-760-1
Alignment Scores:
Pred. No.: 0 Length: 3232
Score: 4203.00 Matches: 818
Percent Similarity: 99.88% Conserved: 1
Best Local Similarity: 99.76% Mismatches: 1
Query Match: 87.60% Indels: 0
DB: 1 Gaps: 0
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RESULT 9

US 09 026 459a 2/2

Sequence 2: Application US/09048760

Patent No. 6496741

GENERAL INFORMATION:

APPLICANT: X0, Renat Li

APPLICANT: 807, Shi Xue

TITLE OF INVENTION: Broad Spectrum Tumor Suppressor Groups, Gene Products and

METHODS FOR Tumor Suppressor Gene Therapy.

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pentair & Edwards

STREET: 1115 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: U.S.A.

ZIP: 10036, 2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-PCs/MS-PCs

SOFTWARE: Patent In Release #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/048,760

FILING DATE: 19940425

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Polissant, Brian M

REGISTRATION NUMBER: 28,412

REFERENCE/WORK NUMBER: 7409, 025, 999

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790, 0000

TELEFAX: (212) 869, 9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 4242 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: double

RELEVANCE: not relevant

MOLECULE TYPE: DNA

US 09 026 459a 2

Alignment Summary:

| Prod. No.: | 0 | Length: | 4242 |
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| Sequences: | 4204, 00 | Matches: | 818 |
| Percent Similarity: | 99.88% | Conservativity: | 1 |
| Best Local Similarity: | 99.78% | Mismatches: | 0 |
| Query Match: | 87.60% | Indels: | 0 |
| DB: | 1 | Gaps: | 0 |

US 09 026 459a 1 (1 928) x US 09 048 760 2 (1-4242)

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 DB 2810 TCACCTGCAACACCCAC 2751
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736 GluGluThrPheLysAlaValLeuLysLys--- 745
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2287 AAAAATAAATAATGACTTTGAAATCAATGACTTGAAGTATGACATGACAAAGCAACA 2346
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776 --- ProProThrLeuSerProLeuProHisThrProHisThrProHisThrProHisThr 791
2467 CATAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2517
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2518 CAAAGTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2562
811 SerProLysLysLeuSerGluGlyGluProThrProThrLysMetThrProArgSerArg 830
2563 CCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2604
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RESULT 15

US 08 152 721B 1

Sequence 1, Application US/08152721B

Patent No. 5962315

GENERAL INFORMATION:

APPLICANT: Livingston, David M.

APPLICANT: Ewen, Mark E.

```

TITLE OF INVENTION: DNA Encoding p107 Tumor Suppressor and
TITLE OF INVENTION: Related Polypeptides
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESS: CHATEL, HALL & STEWART
STREET: 53 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2891
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/152,721B
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pasternack Esq., Sam
REGISTRATION NUMBER: 29,576
REFERENCE/DOCKET NUMBER: 181411 01101V
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-5000
TELEFAX: (617) 248-4000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2808 base pairs
TYPE: nucleic acid
STRANDEDNESS: Both
TOPOLOGY: Linear
MOLECULE TYPE: cDNA
HYPOTHEetical: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: cDNA encoding p107
US-08-152-721B-1

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Alignment Scores:
Seq. No.: 1,40-65 Length: 2808
Score: 764.00 Matches: 246
Percent Similarity: 48.17% Conservations: 140
Best Local Similarity: 24.97% Mismatches: 269
Query Match: 15,90% Indels: 340
DB: 2 Gaps: 40
US-09-026-459A-51 (1-938) x US 08 152 721B 1 (1-2808)

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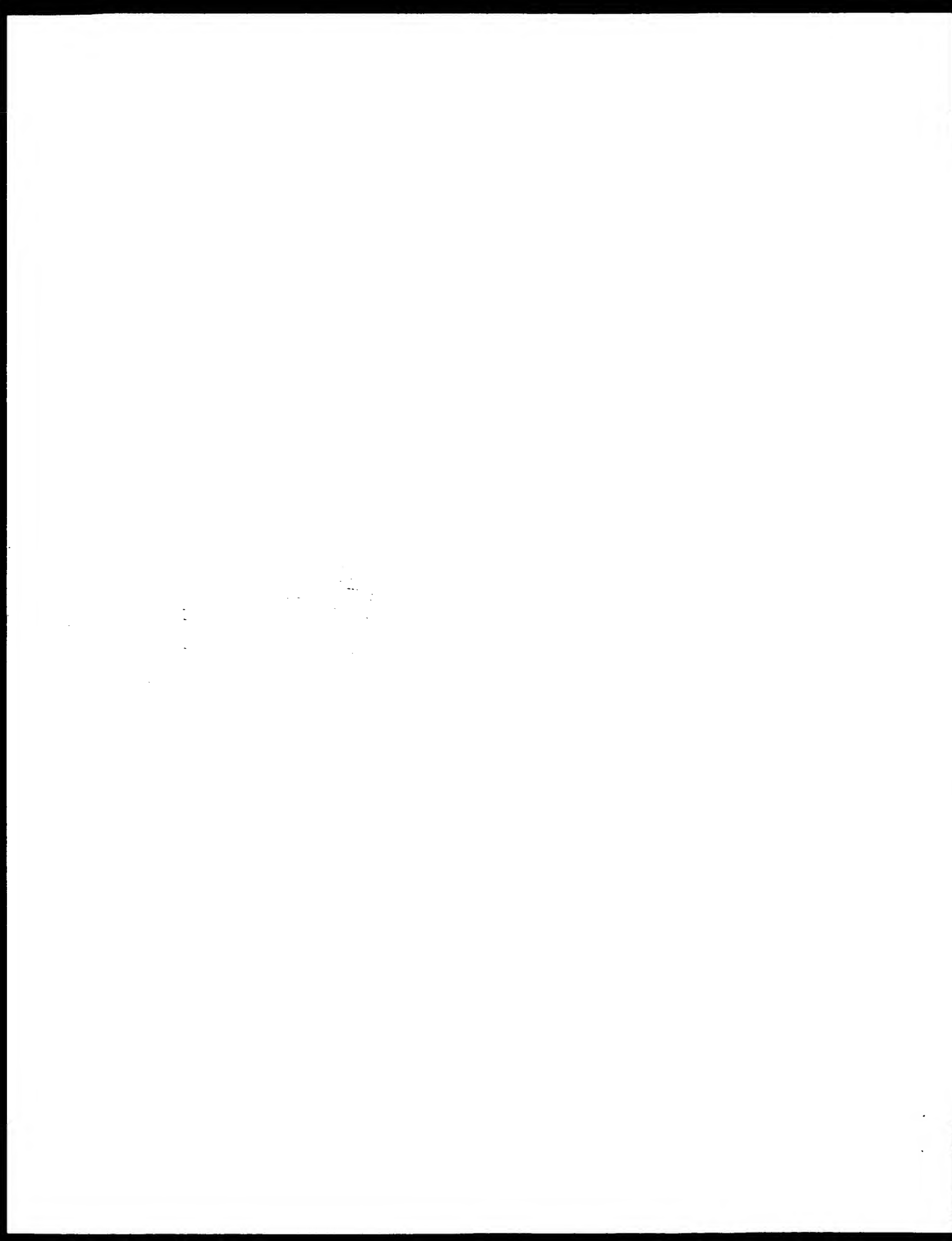
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QY 164 ---LysLeuGluArgThrCysGluLeuLeuLysThrLeuThrLeuProSerSerSer 182
DB 64 CCAAGTTATCAACA-----AGGAGAAAGAGAGAGAGAGATTC 102
QY 183 ThrGluLeuAsnSerAlaLeuValLeuLysValSerThrPheThrPheLeuLeuAlaLys 202
DB 103 TGCAGTCTAAGGAT-----CTGTTTAATTTCTGTGGACACTTTTGTGTTAATAAAG 156
QY 203 GlyGluValLeuGluMetGluAspAspLeuValLeuSerPheGluLeuLeuLeuLysVal 222
DB 157 GGTAAATTTCCGATGATGGGATGACCTTAAGCAATCAATCAATCAATCAATCAATCA 216
QY 223 LeuAspTyrPheLeuLys-----LeuAspPhe 241
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QY 232 ProMetLys LeuLysGluProTyrGlySerAlaValLeuLeuLeuLeuLeuLeuLeu 250
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| QY | 776 | --ProPheThrLeuSerProIlePheHisIleIleProArgSerProTyrLys | 791 |
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| QY | 792 | PheProSerSerProLeuArgTyrIle--ProGlyTyrAsnDLeuTyrTrpSerProLeuLys | 810 |
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| QY | 811 | SerProTyrLysIleSerGluGlyLeuProIleProThrProThrLysMetThrProArgSerArg | 830 |
| D6 | 2564 | TCTGCTGATCAAAATCGCTCTATCGCTT-----ACACCAAGCAAGCGCT | 2604 |
| QY | 831 | IleLeuValSerIleGlyLysSerPheGlyThrSerCLeuLysPheGluLysIleAsnGln | 850 |
| D6 | 2695 | CTGATGCTATAGTTCAAATGGTAGG-----GCTTCTAAGCACTTGAAGATATCAACAAC | 2658 |
| QY | 851 | MetValTyrAsnSerASP-----ArgValIleuLysArgSerAlaGluGly | 865 |
| D6 | 2659 | ATGATANAGAGAGGTGACATGAGAACCAAGCAAGGAGGATATAGCATCATGATATGCA | 2718 |
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Search completed: January 1st, 2003, 05:39:15
Job time : 164.79 secs




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: INFORMATION FOR SEQ ID NO: 2:
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: SEQUENCE CHARACTERISTICS:
:   LENGTH: 2394 base pairs
:   TYPE: nucleic acid
:   STRANDEDNESS: double
:   TOPOLOGY: linear
:   MOLECULE TYPE: DNA (cna)
:   DIS ON 204-429.2

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Attainment Scores:

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| Percent Similarity: | 96.66% | Conservative: | 0 |
| Best Local Similarity: | 96.66% | Mismatches: | 0 |
| Query Match: | 96.4% | Indels: | 1 |
| REP: | 1 | Gaps: | 1 |

US 09 026 459A-41 (1-897) x US-08-204-229-2 (1-2994)

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QY 400 AspIleGlyTyrIlePheLysGlyPheAlaLysAlaValGlyGlyCysValGlu 409
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QY 470 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProTyrIleLeuAsnVal 489
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RESULT 4
US-09-315-113-3
Sequence 3, Application US/09315113
Patent No. 6379927
GENERAL INFORMATION:
APPLICANT: Antelman, Douglas
Gregory, Richard J.
Wills, Kenneth N.
TITLE OF INVENTION: Tissue Specific Expression of Retinoblastoma Protein
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/315,113
FILING DATE: 15 May 1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/801 092
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Fells, Reece A.
REGISTRATION NUMBER: 35,136

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78 2659 AATTCAGAAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2718
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82 2719 ACAAATGCTGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 2778
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84 850 GlySerAspLeuAlaAspGlySerLysHisLeuProGlyLysLeuProLysPheGlnLys 869
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Db 2779 GATCATGATGAAGCATATGAGTAAGTAAGTAAGTAAGTAAGTAAGTAAGTAAG 2838
Gy 870 LeuAlaGluMetThrSerThrArgTrpArgMetGlnGluLysMetAsnAspSerMet 889
Db 2839 CTGGCAAAAAGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2898
Gy 890 AspThrSerAsnLysGlnGluLys 897
Db 2899 GATACTCAACAACAGCAAGCAAGCAAA 2922

RESULT 8
US-08-038-760-1
: Sequence 1, Application US/08038760
: Patent No. 5496741
: GENERAL INFORMATION:
: APPLICANT: Xu, Hong Ji
: APPLICANT: Hu, Shi Xue
: APPLICANT: Benedict, William F.
: TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
: METHODS OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC DOS/MS DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/038,760
: FILING DATE: 1998.125
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: POISSANT, Brian M
: REGISTRATION NUMBER: 28,462
: REFERENCE/DOCKET NUMBER: 7409-025-999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-9741/8864
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4232 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: double
: TOPOLOGY: not relevant
: MOLECULE TYPE: DNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 19..2469
US-08-038-760-1

Alignment Scores:
Pred. No.: 0 Length: 4232
Score: 4218.00 Matches: 820
Percent Similarity: 100.00% Conservat: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 90.97% Indels: 0
DH: 1 Gaps: 0

US-09-026-459A-41 (1-897) x US-08-038-760-1 (1-4232)
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Db 7 GACCAAGATGAGATGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 66
Gy 98 HisLysPheThrAsnLeuLeuLysGlnLeuAspThrSerThrLysValAspAsnAlaMet 117

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480 488 1yt'yysValIleGluSerPheIleLysAlaGluGlyAsnLeuThrArgGluMetIleLys 517
481 1970 1A'AAATGATCGAAAGATTTTATCAAGT'AGAAAGCAACTTGACAAAGAGAAATGATAAA 1911
482 518 HistLeuGluArgCysGluHisArgIleMetGluSerLeuAlaIleProLeuSerAspSerPro 537
483 1910 2ATTTAGAACAGTACGACAAACGAAATCAAGAAATCAAGAAATCCCTTCCATGGCTCTCAGATTCACCT 1851
484 548 LeuPheAspLeuIleLysGluSerLysAspArgLysIleProThrAspHisLeuGluSer 557
485 1851 1AATTCATCTTAAATCTTCTCCAGAAATATCATGACACTGGACGACGATATGATCTTTCT 1741
486 568 ArgValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAspAla 597
487 1741 1CGTGAACATCCCAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1671
488 598 AlaThrGluAlaThrSerAlaPheIleThrGluLysProLeuLysSerThrSerLeuSer 617
489 1671 1GACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAACAAAC 1611
490 618 LeuPheLysLysLysValIleArgAlaAspArgLeuAspArgLeuAspArgLeuAspArg 637
491 1611 1CTTTTATTAATAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1551
492 648 LeuLeuSerGluHisProGluGluGluGluHisIleIleIleThrLeuGluHisThrArg 657
493 1551 1CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1491
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495 1491 1GAAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1431
496 678 1ytGlyIleCysLysValIleAsnIleAspGluLysPheLysIleIleValThrAlaIle 697
497 1431 1ATGATATATGAAATGAAATATGAAATATGAAATATGAAATATGAAATATGAAATATGAA 1371
498 698 LysAspLeuProHisAlaValGluGluThrPheLysArgValLeuIleLysGluLeu 717
499 1371 1AAGCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1311
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505 1191 1CTTAAAGTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1131
506 778 LeuLysSerProTyrGlyIleSerIleGlyLeuProThrProThrLysMetThrProArg 797
507 1131 1CTAAGAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1071
508 798 SerArgIleLeuValSerIleGlyIleGluSerPheClyThrSerGluLysPheClyHis 817
509 1071 1CAAGAAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1011
510 818 AsnIleMetValCysAsnSerAspArgValLeuLysArgSerAlaGluGlySerAsnPro 837
511 1011 1AATCTAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 951
512 838 ProLysProLeuLysLysLeuArgPheAspIleGluGlySerAspGluAlaAspGlySer 857

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Db 950 CCTAAACACATGAAAAAATACGCTTTATATGAGAGAGACAGATGAAACATGAAAT 891
QY 958 LysHisLeuProGlyCysSerLysPheCysGluGlySerAlaGluMetThrSerThrArg 877
Db 960 AATCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 831
QY 878 ThrArgMetGluLysGlySerMetAspAspSerMetAspThrSerAsnLysGluLeuLys 897
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RESULT 10
US-08-470-091-1
: Sequence 1, Application US/08470091
: Patent No. 5913236
: GENERAL INFORMATION:
: APPLICANT: Xu, Hong Ji
: APPLICANT: Hu, Shi-Xue
: APPLICANT: Benedict, William F.
: TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and
: TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
: NUMBER OF SHOWNCHS: 3
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036-2711
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: MS-DOS
: SOFTWARE: Patent in Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/470,091
: FILING DATE: JUN-16-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US/08/038,760
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Poissant, Brian M.
: REGISTRATION NUMBER: 28,462
: PRACTICE/AGENT NUMBER: 7409-025-999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790-9090
: TELEFAX: (212) 869-9741/8864
: TELEX: 66141 PENNIE
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3242 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: not relevant
: MOLECULE TYPE: DNA
: PHATURE:
: NAME/KEY: GDS
: LOCATION: 19..2469
US-08-470-091-1
Alignment Scores:
pred. No.: 0 Length: 1232
Score: 4213.60 Matches: 820
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 90.97% Indels: 0
DB: 2 Gaps: 0
US-08-026-459a-41 (1-897) x US-08-470-091-1 (1-1232)
QY 78 AspLeuAspGluMetSerPheThrGluLeuGluLysAsnIleGluIleSerVal 97

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 102 100 TTTTAAATTTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 126
 103 118 SerAspLeuLeuLysGluLeuLysValLeuPheAlaLeuPheSerLysGluLeuArgThr 147
 104 120 TCAAGACATGCTGCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 186
 105 138 GAGGCTGCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 157
 106 148 TCAAGACATGCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 246
 107 158 LeuValLeuLysValSerThrPheLeuLeuLysGluLeuLysGluLeuLysGluLeuMet 177
 108 247 TTTGCTGCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 306
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 111 198 LeuSerProMetLeuLeuLysGluLeuPheLysThrAlaValLeuPheLeuAsnGly 217
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 113 218 SerProArgThrProArgThrGluLeuAspArgSerAlaArgThrAlaLysGluLeuGlu 237
 114 427 TCAAGACATGCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 486
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 117 258 LysAsnValThrPheLysAsnPheLeuProPheMetAsnSerLeuGlyLeuValThrSer 277
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 136 1087 TCAAGACATGCTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1146

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 101 1147 TGGGCTCTTGAGGTGTGAATGGTACATATAGTACAGAGTACATATAGAAATCTTGATCT 1206
 102 478 GlyThrAspLeuSerPheProThrPheLeuAsnValLeuAsnLeuLysAlaPheAspPhe 497
 103 1207 GCAACACAGATTTGCTTGGCTATGGATTCGAAATTCGAAATTCGAAATTCGAAATTCGAA 1266
 104 498 TyrLysValIleGluSerPheIleLysAlaGluLeuValAsnLeuThrAlaGluMetIleLys 517
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 108 538 LeuPheAspLeuLeuLysGluSerLysAspArgLeuGlyProThrAspHisLeuGluSer 557
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 112 578 ProValArgSerProLysLysLysGlySerThrThrArgValAsnSerThrAlaAsnAla 597
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 116 618 LeuPheTyrLysLysValTyrArgLeuAlaTyrLeuArgLeuAsnThrLeuLysGluArg 637
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 127 1927 TAAGATCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1986
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 130 758 ProTyrLysProSerProSerProSerProSerProSerProSerProSerProSerPro 777
 131 2047 CTTTACAGTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2106
 132 778 LeuLysSerProTyrLysIleSerGluGlyLeuProThrProThrLysMetThrProArg 797
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 134 798 SerArgIleLeuValSerIleGlyLysSerIleGlyLysThrSerGluLysThrIleLys 817
 135 2167 TCAAGATCTTCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2226

US 07 Jan 96.2.1

Alignment Scores:

Prod. No.: 6,076,47 Length: 2808
 Score: 748.00 Matches: 247
 Percent Similarity: 38.27% Conservative: 140
 Best Local Similarity: 25.98% Mismatches: 268
 Query Match: 16.58% Indels: 340
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US 09 26 459A-41 (1-897) x US-07-708 952-1 (1-2808)

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 QY 130 LysLeuGlnArgThrCysGlnLeuLleTyrLeuThrGlnProSerSorSoriLeuSer 151
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 QY 152 ThrGlnLleAsnSerAlaLeuValLeuLysValSerTyrPheThrPheLeuLeuAlaLys 171
 DB 104 TCCAGGTTAAGCAI-----CAGTTAAATTCCTGTTGGACACATTTTGTATATACTAAG 156
 QY 172 GlyGlnValLeuGlnMetGlnAspLeuValLleSerPheGlnLeuMetLeuCysVal 191
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 QY 192 LeuAspTyrPheThrLys-----LeuSerPro 200
 DB 217 TTGATCTGATTTTTCGATGCGATTATATGCGCAAAATAGCAAAAGCTTGTAAATGCA 276
 QY 200 ProMetLeu---LeuLysCysProPheTyrThrAlaValLleProLleAsnLysSerPro 219
 DB 258 TCAATTTAAAGGTTTACCATCTGATTTTCTACTGCTGACATTTACGGCTTCTCAAGAGCCA 336
 QY 220 ArgThrProAlaGlnGlnAsnArgSerAlaArgLleAlaLysGlnLeuLysLysAsp 239
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 QY 340 ProHis----- 341
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 DB 850 GAATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 111
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 QY 491 AsnLeuLysAlaLlePheAspPheCysValLleGlnSerPheLysLysLysLysLysLysLys 510
 DB 1180 AACTTGAACCATTTTATTAAGGTTATTAAGGTTATTAAGGTTATTAAGGTTATTAAGGTTATTA 1239
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 QY 548 ----- 548
 DB 1420 GATATCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1479
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 QY 574 MetTyrLeuSerProVal-----ArgSerProLysLys 584

[illegible]

research completed: January 19, 2003, 05:30:16
 job time : 176.027 secs

1. The first part of the document is a list of the names of the persons who were present at the meeting. The names are listed in alphabetical order.

2. The second part of the document is a list of the topics that were discussed at the meeting. The topics are listed in alphabetical order.

3. The third part of the document is a list of the actions that were taken at the meeting. The actions are listed in alphabetical order.

4. The fourth part of the document is a list of the decisions that were made at the meeting. The decisions are listed in alphabetical order.

5. The fifth part of the document is a list of the recommendations that were made at the meeting. The recommendations are listed in alphabetical order.

23 47 5AATTAGATGATGCTGCTTCACTTTTATCGAGCTACAGAAAAACATAGAAATCAGTGT 296
100 6 5AATCAGACAGACAGAGCGGTCACCTTATCAGGACAGAAAAACATAGAAATCAGTGT 65
24 27 5ATAAATGTTTAAATTTAATAAAGAAATTTGATACGAGTACAAAGTTGATATGCTAT 356
100 66 5ATAAATGTTTAAATTTAATAAAGAAATTTGATACGAGTACAAAGTTGATATGCTAT 125
25 357 5TCAAGACATGTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 416
100 126 5TCAAGACATGTCAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 185
26 417 5ATGAGAAATTAATATATTTTGAACAAAGAGAGTTGATGATGATGATGATGATGATGAT 476
100 186 5ATGAGAAATTAATATATTTTGAACAAAGAGAGTTGATGATGATGATGATGATGATGAT 245
27 477 5ATGAGAAATTAATATATTTTGAACAAAGAGAGTTGATGATGATGATGATGATGATGAT 536
100 246 5ATGAGAAATTAATATATTTTGAACAAAGAGAGTTGATGATGATGATGATGATGATGAT 305
28 537 5AAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 596
100 406 5AAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 365
29 597 5ACTTCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 656
100 466 5ACTTCAATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 425
30 657 5TCAATGAGAAATTAATATATTTTGAACAAAGAGAGTTGATGATGATGATGATGATGAT 716
100 426 5TCAATGAGAAATTAATATATTTTGAACAAAGAGAGTTGATGATGATGATGATGATGAT 485
31 717 5AAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 776
100 486 5AAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 545
32 777 5AAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 836
100 546 5AAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 605
33 837 5AATGAGAAATTAATATATTTTGAACAAAGAGAGTTGATGATGATGATGATGATGATGAT 896
100 606 5AATGAGAAATTAATATATTTTGAACAAAGAGAGTTGATGATGATGATGATGATGATGAT 665
34 897 5AAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 956
100 666 5AAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 725
35 957 5AATGAGAAATTAATATATTTTGAACAAAGAGAGTTGATGATGATGATGATGATGATGAT 1016
100 726 5AATGAGAAATTAATATATTTTGAACAAAGAGAGTTGATGATGATGATGATGATGATGAT 785
36 1017 5AATGAGAAATTAATATATTTTGAACAAAGAGAGTTGATGATGATGATGATGATGATGAT 1076
100 786 5AATGAGAAATTAATATATTTTGAACAAAGAGAGTTGATGATGATGATGATGATGATGAT 845
37 1077 5AATGAGAAATTAATATATTTTGAACAAAGAGAGTTGATGATGATGATGATGATGATGAT 1136
100 846 5AATGAGAAATTAATATATTTTGAACAAAGAGAGTTGATGATGATGATGATGATGATGAT 905
38 1137 5AATGAGAAATTAATATATTTTGAACAAAGAGAGTTGATGATGATGATGATGATGATGAT 1196
100 906 5AATGAGAAATTAATATATTTTGAACAAAGAGAGTTGATGATGATGATGATGATGATGAT 965
39 1197 5AATGAGAAATTAATATATTTTGAACAAAGAGAGTTGATGATGATGATGATGATGATGAT 1256
100 966 5AATGAGAAATTAATATATTTTGAACAAAGAGAGTTGATGATGATGATGATGATGATGAT 1025
40 1257 5AATGAGAAATTAATATATTTTGAACAAAGAGAGTTGATGATGATGATGATGATGATGAT 1316
100 1026 5AATGAGAAATTAATATATTTTGAACAAAGAGAGTTGATGATGATGATGATGATGATGAT 1085

QY 1317 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1376
DB 1086 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1145
QY 1377 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1436
DB 1146 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1205
QY 1437 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1496
DB 1206 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1265
QY 1497 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1556
DB 1266 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1425
QY 1557 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1616
DB 1326 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1485
QY 1617 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1676
DB 1386 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1445
QY 1677 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1736
DB 1446 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1505
QY 1737 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1796
DB 1506 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1565
QY 1797 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1856
DB 1566 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1825
QY 1857 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1916
DB 1626 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1885
QY 1917 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1976
DB 1686 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1945
QY 1977 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 2036
DB 1746 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1895
QY 2037 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 2096
DB 1806 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1865
QY 2097 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 2156
DB 1866 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1925
QY 2157 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 2216
DB 1926 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 1985
QY 2217 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 2276
DB 1986 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 2045
QY 2277 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 2336
DB 2046 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 2105
QY 2337 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 2396
DB 2106 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 2165
QY 2397 ATGCATTCAAAATTTTACGAAATTTTGAATGACAAATTTTTCATATGCTTTTATTTGAC 2456

FEATURE:

NAME/KEY: CDS

Accession: 139..2922

Size: 369,338 bp

Query Match: 76.8%; Score 2658.8; DB 2: Length 2995;

Best Local Similarity 96.7%; Pred. No. 0;

Matches 2764; Conservative 0; Mismatches 2; Indels 93; Gaps 1;

97 2 GTGTCATGCGCGCCCAAAACCTCGGAAAAACGGCCGACCGCCGCGCGCGCGCGCG 61
 100 |||||
 101 134 GTGTCATGCG 193
 102 |||||
 103 105 AAAG 121
 104 |||||
 105 134 AAAG 253
 106 |||||
 107 122 AG 181
 108 |||||
 109 134 AG 313
 110 |||||
 111 122 AG 233
 112 |||||
 113 124 AG 373
 114 |||||
 115 233 AG 233
 116 |||||
 117 174 AG 433
 118 |||||
 119 233 AG 268
 120 |||||
 121 433 AG 493
 122 |||||
 123 233 AG 328
 124 |||||
 125 433 AG 553
 126 |||||
 127 429 AG 388
 128 |||||
 129 564 AG 613
 130 |||||
 131 433 AG 448
 132 |||||
 133 614 AG 673
 134 |||||
 135 449 AG 508
 136 |||||
 137 674 AG 733
 138 |||||
 139 569 AG 568
 140 |||||
 141 734 AG 793
 142 |||||
 143 769 AG 628
 144 |||||
 145 794 AG 853
 146 |||||
 147 629 AG 688
 148 |||||
 149 854 AG 913
 150 |||||
 151 689 AG 748
 152 |||||
 153 914 AG 973
 154 |||||
 155 749 AG 808
 156 |||||
 157 974 AG 1033
 158 |||||
 159 809 AG 868
 160 |||||
 161 1034 AG 1093
 162 |||||

QY 869 AACGATACGAAGAAATTTATCTTAAATAAAGATCTAGATCAAGATTATTTTGGATC 928
 DB |||||
 DB 1094 AACGATACGAAGAAATTTATCTTAAATAAAGATCTAGATCAAGATTATTTTGGATC 1154
 QY 929 ATGATAAAACCTTCACACATGATTCATACACAGATTTTGAACACACAGACAAATATATGAA 988
 DB |||||
 DB 1154 ATGATAAAACCTTCACACATGATTCATACACAGATTTTGAACACACAGACAAATATATGAA 1214
 QY 989 AAATTAACCTTCACACATGATTCATACACAGATTTTGAACACACAGACAAATATATGAA 1048
 DB |||||
 DB 1214 AAATTAACCTTCACACATGATTCATACACAGATTTTGAACACACAGACAAATATATGAA 1274
 QY 1049 TGACACTATTCACACATGATTCATACACAGATTTTGAACACACAGACAAATATATGAA 1108
 DB |||||
 DB 1274 TGAACACTATTCACACATGATTCATACACAGATTTTGAACACACAGACAAATATATGAA 1334
 QY 1109 ATCTGATTTTCTATTTTAACTACACAGATTTTGAACACACAGACAAATATATGAA 1168
 DB |||||
 DB 1334 ATCTGATTTTCTATTTTAACTACACAGATTTTGAACACACAGACAAATATATGAA 1394
 QY 1169 TGAAGCATATGACATACATTTTAAACAGACAAATTTTGAACACACAGACAAATATATGAA 1228
 DB |||||
 DB 1394 TGAAGCATATGACATACATTTTAAACAGACAAATTTTGAACACACAGACAAATATATGAA 1454
 QY 1229 TGAACACTATTCACACATGATTCATACACAGATTTTGAACACACAGACAAATATATGAA 1288
 DB |||||
 DB 1454 TGAACACTATTCACACATGATTCATACACAGATTTTGAACACACAGACAAATATATGAA 1514
 QY 1289 CCATGCTTAAATTCACACAGACAAATTTTGAACACACAGACAAATTTTGAACACAGAC 1348
 DB |||||
 DB 1514 CCATGCTTAAATTCACACAGACAAATTTTGAACACACAGACAAATTTTGAACACAGAC 1574
 QY 1349 ACAACATTTTCTATTTTAACTACACAGATTTTGAACACACAGACAAATTTTGAACACAG 1408
 DB |||||
 DB 1574 ACAACATTTTCTATTTTAACTACACAGATTTTGAACACACAGACAAATTTTGAACACAG 1634
 QY 1409 GTCACACTATTCACACATGATTCATACACAGATTTTGAACACACAGACAAATTTTGAACACAG 1468
 DB |||||
 DB 1634 GTCACACTATTCACACATGATTCATACACAGATTTTGAACACACAGACAAATTTTGAACACAG 1694
 QY 1469 ATCTGATTTTCTATTTTAACTACACAGATTTTGAACACACAGACAAATTTTGAACACAG 1528
 DB |||||
 DB 1694 ATCTGATTTTCTATTTTAACTACACAGATTTTGAACACACAGACAAATTTTGAACACAG 1754
 QY 1529 AAGCAACTTCACACAGACAAATTTTGAACACACAGATTTTGAACACACAGACAAATTTTGAACACAG 1588
 DB |||||
 DB 1754 AAGCAACTTCACACAGACAAATTTTGAACACACAGATTTTGAACACACAGACAAATTTTGAACACAG 1814
 QY 1589 AATCTGATTTTCTATTTTAACTACACAGATTTTGAACACACAGACAAATTTTGAACACAG 1648
 DB |||||
 DB 1814 AATCTGATTTTCTATTTTAACTACACAGATTTTGAACACACAGACAAATTTTGAACACAG 1874
 QY 1649 GACAAGCAACTTCACACATGATTCATACACAGATTTTGAACACACAGACAAATTTTGAACACAG 1708
 DB |||||
 DB 1874 GACAAGCAACTTCACACATGATTCATACACAGATTTTGAACACACAGACAAATTTTGAACACAG 1944
 QY 1709 ATCTGATTTTCTATTTTAACTACACAGATTTTGAACACACAGACAAATTTTGAACACAG 1768
 DB |||||
 DB 1934 ATCTGATTTTCTATTTTAACTACACAGATTTTGAACACACAGACAAATTTTGAACACAG 1994
 QY 1769 CTATCTGATTTTCTATTTTAACTACACAGATTTTGAACACACAGACAAATTTTGAACACAG 1828
 DB |||||
 DB 1994 CTATCTGATTTTCTATTTTAACTACACAGATTTTGAACACACAGACAAATTTTGAACACAG 2054
 QY 1829 AGAAGCAACTTCACACATGATTCATACACAGATTTTGAACACACAGACAAATTTTGAACACAG 1888
 DB |||||
 DB 2054 AGAAGCAACTTCACACATGATTCATACACAGATTTTGAACACACAGACAAATTTTGAACACAG 2114
 QY 1889 ATCTGATTTTCTATTTTAACTACACAGATTTTGAACACACAGACAAATTTTGAACACAG 1948
 DB |||||
 DB 2114 ATCTGATTTTCTATTTTAACTACACAGATTTTGAACACACAGACAAATTTTGAACACAG 2174
 QY 1949 TATCTGATTTTCTATTTTAACTACACAGATTTTGAACACACAGACAAATTTTGAACACAG 2008

XX W 98-09-1-A2.
 XX 19-FEB-1998; 98W0-0504041.
 XX 20-FEB-1997; 97US 0048118.
 XX (BAYLOR) BAYLOR COLLEGE MEDICINE.
 XX (TEXAS) UNIV TEXAS SYSTEM.
 XX Protein: Wt: 80 S: N: H: Chem: V:
 XX WPI: 1998-480788/41.
 XX P-ESC-B: AAW69368.
 XX Metinblastoma suppressor protein with N-terminal modification -
 XX inhibiting cellular proliferation, particularly cancer
 XX Class 22; Page 166-170; 249pp; English
 XX This sequence encodes a modified retinoblastoma tumour suppressor
 XX protein (R1SP) of the invention, the proteins can be used for inhibiting
 XX cellular proliferation, when coadministered with a p53 protein. The R1SPs
 XX can be used for treating diseases characterised by abnormal cellular
 XX proliferation, particularly cancers. The R1SPs have a broader spectrum of
 XX activity than wild type R1SPs.
 XX Sequence 3266 bp; 1092 A; 602 C; 574 G; 998 T; 0 other;
 XX
 XX Alignment Scores:
 XX Fred. No.: 0 Length: 3266
 XX Score: 4278.00 Matches: 832
 XX Percent Similarity: 100.00% Conservative: 6
 XX Best local Similarity: 100.00% Mismatches: 0
 XX Query Match: 100.00% Indels: 0
 XX Gap: 19 Gaps: 0
 XX
 XX us-09-026-459a-35 (1-832) x AAV58444 (1-3266)
 XX 1 MetLeuThrGlyIleCysIlePheIleAlaValAspIleuAspGluMetSerPheThr 20
 XX 7 AIGRTIGGGAAICIGIAICITATATGACAGCAGCTGACCTAGATCAGAGICGCTICACI 66
 XX 21 PheThrGluLeuGluLysAsnIleGluIleSerValHisLysPhePheAsnLeuLys 40
 XX 67 TTTACIGAGCIGACAAACAAACATAGAAATCAGCTGCTCCATAAATCTTTAACTTACIAAAA 126
 XX 41 GluIleAspThrSerThrLysValAspAsnAlaMetSerArgIleuLysLysIleAsp 60
 XX 127 CAATTCATACACATCAAAATGATATGCTATATATATATATATATATATATATATATATAT 186
 XX 61 ValIlePheAlaIlePheSerLysLeuGluArgThrCysGluLeuIleIleIleLeuThrGln 80
 XX 187 GATGTTGTCACCTCTCAGCAAAATGAGAAAGGACATGACCTTATATATATATATATATAT 246
 XX 81 ProSerSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSerIleIle 100
 XX 247 CTAACAGCTGCAATCIGATCAAAATATATATGCTATGCTATGCTATGCTATGCTATGCTAT 306
 XX 111 ThrPheLeuAlaIleCysIleGluValIleuIleMetIleAspIleuValIleSerPhe 120
 XX 337 AATTTTATTAAGTAAAGAGAAATATATATATATATATATATATATATATATATATATAT 366
 XX 121 GluLeuMetIleuCysValIleuAspIlePheIleIleLysLeuSerProMetIleuLys 140
 XX 367 CAGTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 426
 XX 141 GluProIleThrAlaValIlePheIleAsnIleSerProArgThrProArgArgGly 160
 XX 427 CAATCATATAAAACAGCTGAT 486

QY 161 GlnAsnArgSerAlaArgIleAlaIleLysGlnIleuGluAsnAspThrArgIleIleIleGluVal 180
 Db 487 CAGAAATAGCAATGCAAGATAGCAAAACAAATAGAAAAATGATACAAAGAAATATATATATATAT 346
 QY 181 LeuCysLysGluHisGlyCysAsnIleAspGluValLysAsnValTyrThrLysAsnPhe 200
 Db 547 CICTGTAAAGAACATGAAATGAT 606
 QY 201 IleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProIleValThrAla 220
 Db 607 AIAATTTTAT 466
 QY 221 LeuSerLysArgIleGlyCysGluIleLysLeuLysAsnIleAspIleuAspAlaIleuPhe 240
 Db 667 CTITTAAT 726
 QY 241 LeuAspHisAspLysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnAsnThr 260
 Db 727 TTGATCATGATAAAACTCTCAGACIGATATATATATATATATATATATATATATATATATATAT 786
 QY 261 ProArgLysSerAsnLeuAspGluValAsnValIlePheProIleThrProValAla 280
 Db 787 CCAGCAAAAT 846
 QY 281 ThrValMetAsnThrIleGlnGlnLeuMetMetIleuAsnSerAlaSerAspGluPro 300
 Db 847 ACTGTTATGACACTAT 906
 QY 301 SerGluAsnLeuIleSerIlePheAsnAsnCysThrValAsnProLysGluSerIleLeu 320
 Db 907 TCAGAAATCTGAT 966
 QY 321 LysArgValLysAspIleGlyTyrIlePheLysGluLysPheAlaLysAlaValGlyGln 340
 Db 967 AAAAT 1026
 QY 341 GlyCysValGluIleGlySerGlnArgTyrLysGluGlyValArgIleGlyTyrArgVal 360
 Db 1027 GCTTGTCTCAAT 1086
 QY 361 MetGluSerMetLeuLysSerGluGluArgLeuSerIleGlnAsnPheSerLysLeu 380
 Db 1087 ATGCAATCTAT 1146
 QY 381 LeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAla 400
 Db 1147 CTGAATCAGAACATTTTCTAT 1206
 QY 401 ThrTyrSerArgSerThrSerGlnAsnLeuAspSerClyThrAspIleuSerPheProIle 420
 Db 1207 ACATATAGCAAGCAAT 1266
 QY 421 IleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIle 440
 Db 1267 ATTCGAAATGCTTAT 1326
 QY 441 LysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArg 460
 Db 1327 AAGCAAGAGCAATCTGAT 1386
 QY 461 IleMetGluSerLeuAlaIlePheSerAspSerProIlePheAspIleuIleLysGlnSer 480
 Db 1487 ATCATGAAATCTGAT 1446
 QY 481 LysAspArgGluGlyProThrAspHisLeuGluSerAlaCysIleuAsnLeuIleuLeu 500
 Db 1447 AAGCAAGAGCAATCTGAT 1506
 QY 501 GluAsnAsnIleThrAlaValAspMetTyrLeuSerProValArgSerProLysIleGly 520
 Db 1507 CAGTAT 1566
 QY 521 GlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaIle 540

XX 24 Apr 1994 (first entry)
 XX Retinoblastoma gene.
 XX
 XX RB gene product: p105RB protein: cell cycle progression control;
 XX contribution: therapeutic methods: arrest; tumorigenesis;
 XX regulation: physiological processes: blood cell production;
 XX tumorigenesis.
 XX
 XX Homo sapiens SR 40 cell line.
 XX
 XX Key Location/Qualifiers
 XX CHS 149,2945
 XX 28 Apr 94
 XX /note "RB protein"
 XX
 XX W00000267 A.
 XX
 XX 29 APR 1994.
 XX 16 Oct 1992: 9260 US069418.
 XX 17 Oct 1991: 9135 0778510.
 XX (R033) UNIV CALIFORNIA.
 XX
 XX Goodrich LW, Lee EYBP, Lee WB, Wang NP;
 XX WPI: 1994 152462/18.
 XX P 1990; AAK 0544.
 XX
 XX Method of controlling cell cycle progression, uses purified
 XX retinoblastoma protein or fragment, for use in combination with
 XX therapeutic methods to arrest tumorigenesis
 XX
 XX Disclosure: Fig 9; 68pp; English.
 XX
 XX The sequence is that of the retinoblastoma gene which encodes the
 XX retinoblastoma (RB) protein which may be used as part of a method of
 XX controlling cell cycle progression which may be used in combination
 XX with therapeutic methods to arrest tumorigenesis in organisms. The
 XX cell cycle can be reversibly arrested in a convenient and safe
 XX manner. The protein is used in a compo. is relatively inexpensive
 XX and readily obtainable, and shows little or no toxic effects on
 XX healthy cells. It is also compatible with other methods and devices
 XX for regulating certain physiological processes of the body, such as
 XX blood cell prodn. and gamete prodn. Fragments of the protein are
 XX soluble in low concns. of glycerol thus enhancing their value in
 XX pharmaceutical applications.
 XX
 XX Sequence 2994 BP: 974 A: 418 C: 594 G: 808 T: 0 other:
 XX
 XX Alignment Scores:
 XX
 XX Seq. No.: 1
 XX Score: 4274.99
 XX Percent Similarity: 100.00%
 XX Best Local Similarity: 100.00%
 XX Query Matches: 99.88%
 XX Gaps: 14
 XX
 XX Seq. No. 2: 459A (1 832) x AAG41545 (1-2994)
 XX
 XX 2 LeuThrPheLeuValAlaValAspLeuAspGluMetSerPheThrPhe 21
 XX 430 CAGGCGGAAACGCGGAACTTATGCGAGAGTGCACCTAGACAGATGCGTTCACCTTT 489
 XX 22 ThrGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 41
 XX 490 AATGAGTACAGAAAAATAGAAATAGTGTGATATATATATATATATATATATATATAT 549
 XX 42 ThrAspThrSerThrThrValAspAlaMetSerArgLeuLeuLeuLeuLeuLeuLeu 61
 XX

DB 550 ATGATATACAGTACCAAGTTGATAAAGCTATGTCACAAACATGTCAGATGATG 609
 QY 62 LeuPheAlaLeuPheSerLeuGluAlaThrCysGluLeuLeuLeuLeuLeuLeuLeu 81
 DB 610 TTGTTTGACACTTCTTCAAGAAATGGAAGAGAAAGTAAATATATATATATATATATAT 659
 QY 82 SerSerSerThrThrGluThrGluThrGluThrGluThrGluThrGluThrGluThr 101
 DB 670 AATGAGTACAGAAAAATAGAAATAGTGTGATATATATATATATATATATATATATAT 729
 QY 102 PheLeuLeuAlaLysGlyGluValLeuGluMetGluAspAspLeuValLeuSerPheGlu 121
 DB 740 TTTTATATAGCTAAAGCGAAGTATATATATATATATATATATATATATATATATATAT 789
 QY 122 LeuMetLeuGlyValLeuAspThrPheLeuGluGluGluGluGluGluGluGluGlu 141
 DB 790 TTAATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 849
 QY 142 ProTyrThrThrAlaValLeuThrGluThrGluThrGluThrGluThrGluThrGluThr 161
 DB 850 GCTAT 909
 QY 162 AsnArgSerAlaAlaArgAlaAlaLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 181
 DB 910 AACAGAGTGCAGGATAGTAAATATATATATATATATATATATATATATATATATAT 969
 QY 182 CysGlyGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGluGlu 201
 DB 970 TGTAAAGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATGAAATG 1029
 QY 202 ProPheMetAsnSerLeuLeuValThrSerAsnGlyLeuThrGluValGluAlaSer 221
 DB 1040 GCTTAT 1089
 QY 222 SerTyrArgTyrGluGluLeuTyrLeuGlySerSerSerSerSerSerSerSerSer 241
 DB 1090 TCTAAAGCAATACGAG 1149
 QY 242 AspPheAspLysThrLeuGluThrAspSerThrGluThrGluThrGluThrGluThr 261
 DB 1150 GAT 1209
 QY 262 ArgSerSerAsnGluAspGluGluValAsnValThrGluThrGluThrGluThrGlu 281
 DB 1210 GAAAAAT 1269
 QY 282 ValMetAsnThrThrLeuGluThrLeuMetMetLeuLeuAsnSerAlaSerAspGluProSer 301
 DB 1270 GTTATGAACTACTATGCAACAAATATATATATATATATATATATATATATATATAT 1329
 QY 302 GluAsnLeuThrSerTyrPheAsnAspCysThrValAsnProLysGluSerThrLeuLys 321
 DB 1340 GAAAAATGATTTGATTTTAT 1389
 QY 322 ArgValLysAspThrGlyTyrThrPheGlySerGlySerGlySerGlySerGlySer 341
 DB 1390 AGAGTGAAGATATAGAT 1449
 QY 342 CysValGluThrGlySerGluArgTyrLysLeuGlyValArgLeuGlyTyrThrValMet 361
 DB 1450 TGTGTCCAAATGCAATCAACGCAATACAAATGCAATGCAATGCAATGCAATGCAATG 1509
 QY 362 GluSerMetLeuLysSerSerGluGluGluGluGluGluGluGluGluGluGluGlu 381
 DB 1510 GAATTCATGCTTAATATAGAAAGAGAAAGATATATATATATATATATATATATATATAT 1569
 QY 382 AsnAspAsnThrPheHisMetSerLeuLeuAlaCysAlaLeuLeuValMetAlaThr 401
 DB 1570 AATGAGTACAGAAAAATAGAAATAGTGTGATATATATATATATATATATATATATAT 1629
 QY 402 TyrSerArgSerThrSerGluAsnLeuAspSerGlyThrAspLeuSerPheThrPhe 421
 DB 1630 TATATACAAAGTACAT 1689

459 46 459A-35 (1-832) x AAX00737 (1-2995)
QY 2 LeuArgpGlyTyrCysHisPheGluAlaValAspLeuAspGluMetSerPheThrPhe 21
DB 46 TGTGGGGAATGCTGATCTTTTATGCGAGAGCTTGGAGCTATGATGATGCTGCTTCATCTTT 489
QY 2 ThrGluLeuGlnLysAsnIleGluLeuSerValHisLysPhePheAsnLeuLeuLysGlu 41
DB 46 ACTCAAGTACACAAACAAACATAGAAACAGTCTCCATTAATCTTAACTTACIAAAGAA 549
QY 4 IleAspThrSerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysCysAspVal 61
DB 46 AATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGATATGAT 609
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QY 142 ProTyrLysThrAlaValIleProIleAsnGlySerProArgThrProArgLysGln 161
DB 46 CAAATAAAACAGCGTGTATACCGCAATAACGCTCAGCTGGAACATCCAGAGCTGAAACATC 909
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QY 162 TysLysSerThrLysCysLysAspCysValLysAsnValTyrLysLysAsnThrIle 201
DB 46 GTTAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1029
QY 242 ProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValGluAsnLeu 221
DB 46 CAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1089
QY 242 SerLysAspThrLysLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 241
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QY 242 AspHisAspLysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArgThrPro 261
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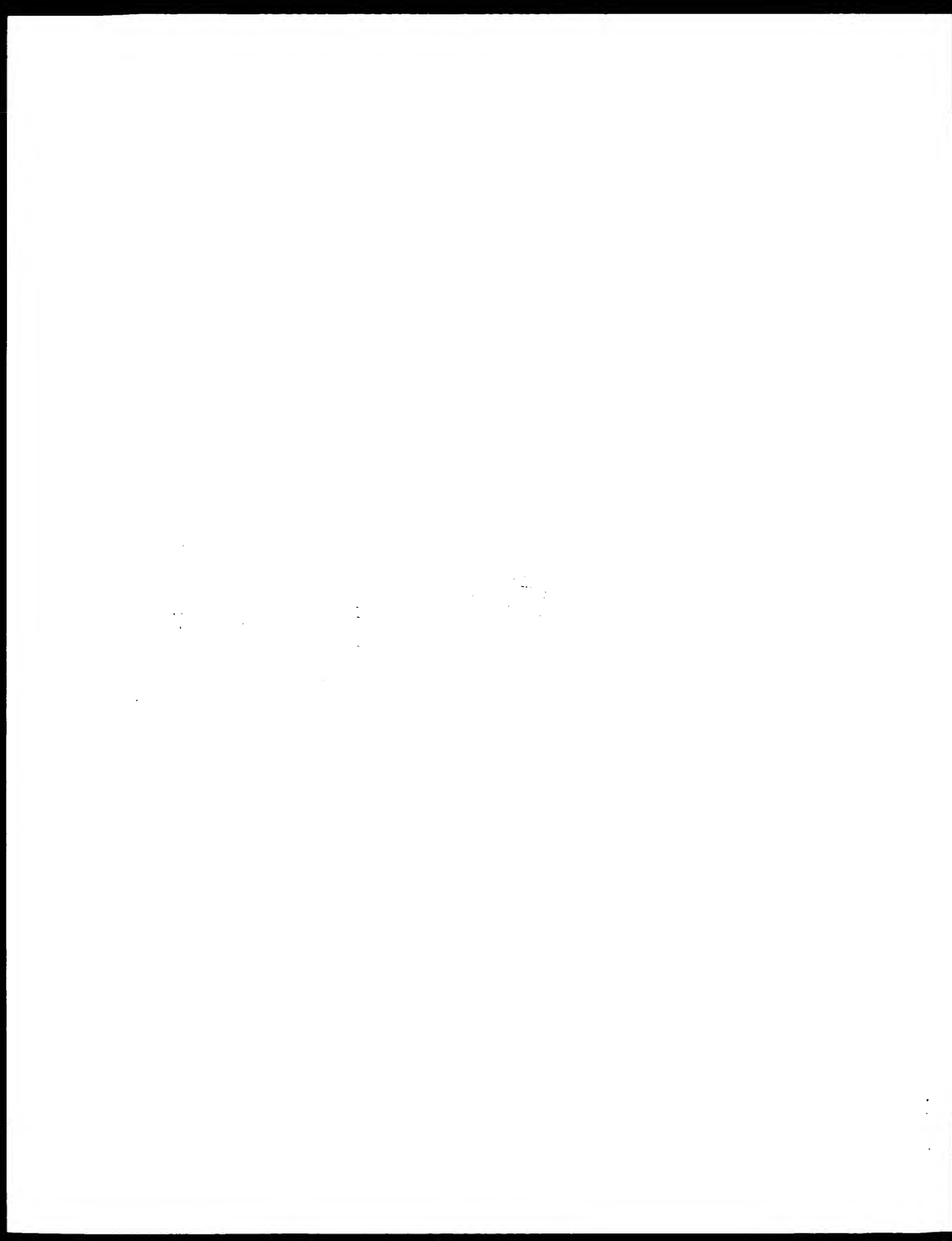
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QY 462 ClusterMetLeuLysSerGluGluGluArgLeuSerIleGlnAsnPheSerLysLeuLeu 381
DB 1516 CAATTCATGCTTAAATTCAGAGAGAGAGAGATTAATCAATCAAAATTTAGCAAACTTCTG 1569
QY 382 AsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThr 401
DB 1570 AATTCACAAATTTTCATATGCTCTTATTTGGCGTGGCTCTTGAGAGTGTAAATGCAACA 1629
QY 402 TyrSerArgSerThrSerGlnAsnSerAspSerGlyThrAspLeuSerPheThrProIle 421
DB 1630 TATAGCAAGATCATCTCAGCAATCTGATCTGTAACAGATTTGCTTCTCCATGATTT 1689
QY 422 LeuAspValLeuAsnLeuLysAlaPheAspPheLysValIleGluSerPheIleLys 441
DB 1690 CTGAATGCTGTAAATTTAAAGGCTTTGATTTTACAAAGTCATCGAAAGTTTATCAAA 1749
QY 442 AlaGlyGlyAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGlnHisArgIle 461
DB 1750 GCACAAAGCAACATGACAAAGAAATCAATAAACAATAGAACGATGCAATCAATCAAA 1809
QY 462 MetLeuSerLeuAlaIlePheLeuSerAspSerPheLeuPheAspLeuIleLysGlnSer 481
DB 1810 ATGGATTCGCTTGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1869
QY 482 AspArgGluGlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuProLeuGln 501
DB 1870 CACTCCAAAGAGCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCACTCA 1929
QY 502 AsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysLys 521
DB 1930 AATAATCACACTGCGAGATATGATATGATGATGATGATGATGATGATGATGATGATGAT 1989
QY 522 SerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGln 541
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QY 562 AlaTyrLeuArgLeuAsnThrLeuGlyGluArgLeuLeuSerGluHisProGluLeuGln 581
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DB 2170 CATATCATCTGGAGCCCTTTTCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2229
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QY 662 SerValPheMetGlnArgLeuLysThrAsnIleLeuGluGlyTyrAlaSerThrArgPro 681
DB 2410 TCGCTCTCAATGAG 2469
QY 682 ThrLeuSerProIlePheHisIleProArgSerProTyrLysPheProSerSerPhe 701
DB 2470 ACCATGACCAATACCTACATTCCTGCAAGGCTTTACAGCTTCTTACATGATGATGAT 2529
QY 702 ArgTyrProLysGlyAsnIleTyrIleSerProLysSerProLysSerProLysSerPro 721
DB 2530 CGAATCTCTGAG 2589

550 ATTGATAACAGTACAAAGTTGATAATGCTATGTCACAGACTTTGAGGAGATGATGTA 609
 62 LeuPheAlaLeuPheSerLysLeuGluAlaThrCysGluLeuLeuLeuThrGlnPro 81
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 740 TTTTATATAATGAAAGATATACAAATGGAATGATGATGATGATTCATTCAG 789
 122 LeuMetLeuLysValLeuAspLysPheIleCysIleuSerProMetLeuLeuLysGln 141
 790 TTAATGCTATGCTGCTGATATATTTATTAATCTCAGCTGCTGATGTCAGAA 849
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 910 AACAGGATGACAGATAGCAAAACAAACATGAAATATATACAAATATATGAAATGTC 969
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 970 TGTAAACAAATGAAATGTAATATATGATGATGATGAAATGTTATTTCAAAAAATTTATA 1029
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 222 SerLysAlaTrpGlyGluIleTrpLeuLysAsnLysAspLeuAspAlaArgLeuPheLeu 241
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 1570 AATGACAAATATATGATATGATATGATATGATATGATATGATATGATATGATATGATATG 1629
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1640 TATATGACAAATATATATGATATGATATGATATGATATGATATGATATGATATGATATG 1689
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 2410 TCGCT 2469
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 2590 GCTTGGCAACACCAACAAAAATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2649
 742 SerPheGlyThrSerGluLysPheGluLysIleAsnGlnMetValLysAsnSerAspArg 761
 2650 TCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2709
 762 ValLeuLysArgSerAlaGluGlySerAsnProIleLysProLeuLysLysLeuArgPhe 781
 2710 GTGCTCAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2769

[illegible]

| | | | |
|----|------|--|------|
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| Q7 | 342 | CysValGlnIleGlySerGlnArgTyrTyrLysGlnGlyValArgLeuTyrTyrArgValMet | 361 |
| Db | 1156 | TGTCTCCAAATGGCATACAGCGATACAAACATGGCAGTACGGCTGCTATACAGACAAATG | 1215 |
| Q7 | 362 | GluSerMetLeuLysSerGlnGlnGluArgLeuSerIleGlnAsnPheSerLysLeuLeu | 381 |
| Db | 1216 | CAATCCATGCTTAATACAGAGAAAGAAAGCATATACCATCAAAATCTTAGCAAAATTCCTG | 1275 |
| Q7 | 382 | AsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValValMetAlaThr | 401 |
| Db | 1276 | ATGCAAAATTTTCATATGCTTTATTTGGTGGTGGTCTTGAGGTTGTATAGGCACCA | 1335 |
| Q7 | 402 | TyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProIle | 421 |
| Db | 1336 | TATACAGCAATACATCTACAAATCTTGATCTCTGCAACAGATTTGCTCTTCCTCAAGAT | 1395 |
| Q7 | 422 | LeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLeuValIleGluSerPheIleLys | 441 |
| Db | 1396 | CTCAATGCTCTTAATTTTAAAGCCTTTGATTTTACAAGTCATCGAAAGTTTATCAAA | 1455 |
| Q7 | 442 | AlaGlnGlyAsnLeuThrArgGlnMetIleLysHisLeuGluArgGlyGlnHisArgIle | 461 |
| Db | 1456 | GCAGAGGCAACTTGACAGAGAGAAATGATAAACATTTAGAACGATGTGAACATCAATC | 1515 |
| Q7 | 462 | MetGlnSerLeuAlaIlePheSerAspSerPheGlnPheAspLeuIleLysGlnSerLys | 481 |
| Db | 1516 | ATGGAAATCCCTTGCATGGCTCTCAGATTCACCTTATTTGATCTCTTAAACAAATCAAG | 1575 |
| Q7 | 482 | AspArgGlnGlyProThrAspHisLeuGlnSerAlaCysProLeuAsnLeuProLeuGln | 501 |
| Db | 1576 | CACGCAAGACGACCAACATCATCACTTGAATCTGCTTGCTGCTTAAATCTTCCTCTACG | 1635 |
| Q7 | 502 | AsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysLysGly | 521 |
| Db | 1636 | AAATATCAATACAGAGAAATATGATGATCTTCTACAGTGAAGATCTCAAAATAAAGAGAT | 1695 |
| Q7 | 522 | SerThrThrArgValAsnSerThrAlaAsnAlaGlnThrGlnAlaIleSerAlaPheGln | 541 |
| Db | 1696 | TCACATACGCTCTAAATCTTACTCCAAATCGCAGACACCAAGCAACCTCAAGCTTCCAG | 1755 |
| Q7 | 542 | ThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeu | 561 |
| Db | 1756 | ACGCAGAACGCAATGAAATCTACCTCTCTCTTCACATCTTATTAATAAAAGACTCTATGCG | 1815 |
| Q7 | 562 | AlaTyrLeuArgLeuAspThrLeuCysGlnArgLeuLeuSerGluHisProGlnLeuGln | 581 |
| Db | 1816 | GGCTATCTCGAGTAATAATTTCTGAAAGCTTCTGCTTGTGAGAGCTGAATATTAACA | 1875 |
| Q7 | 582 | HisIleIleThrPheLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAsp | 601 |
| Db | 1876 | CATATCATCTGGACCTTTTTCAGGCACACCTCTCCAGAAATGAGTATGAACATCATCAGAC | 1935 |
| Q7 | 602 | ArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleGlyLysLysValLysAsnIle | 621 |
| Db | 1936 | AGGCATTTGCAGCAAAATATGATGTGTTTCCATCTGATGCAATGCAATGCAAGACGAAATAT | 1995 |
| Q7 | 622 | AspLeuLysPheLysIleIleValThrAlaIleTyrAsnLeuIleHisAlaValGlnGln | 641 |
| Db | 1996 | GAGCTTAATTCAAATCATGTACAGACATACAGAGATCTCCTCATGCTTCTTCAGAG | 2055 |
| Q7 | 642 | IleThrPheArgValLeuIleIleLysGlnGlnGlnIleTyrAspSerIleIleValThrLysAsn | 661 |
| Db | 2056 | ACATTTAAAGCTGCTTGTATCAAGAGAGAGAGATGATGATATATAGATATATATAAAT | 2115 |
| Q7 | 662 | SerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerThrArgProPro | 681 |
| Db | 2116 | TGGCTCTTCATGACAGACATGAAAAACAAATATTTCCAGTATGCTTCCACACAGAGCTCT | 2175 |
| Q7 | 682 | ThrLeuSerProIleProHisIleProArgSerProTyrLysPheProSerSerProLeu | 701 |
| Db | 2176 | ACCTGTCAAAATACATCATCATCTCTCAAGAGCTTCAAGTTCTCTAGTATACCTTAA | 2235 |




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1922 GTTCAAGAAATATGAAAGGTTTGGATCAAAAGAAAGAGTAGTAGATCTATATAGTA 1980
1981 TTTAAAGAAATATGAAAGGTTTGGATCAAAAGAAAGAGTAGTAGATCTATATAGTA 2040
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DB 3241 GTTTTAAATTAATAAAGGTTGCAAAAGCAATGCAATGCAATGCAATGCAATGCAAT 3300
RESULT 2
AAV58443
ID AAV58443 standard, LNA, 3423 bp.
XX
AC AAV58443;
XX
DI 02-DEC-1998 (first entry)
XX
DE Modified retinoblastoma tumour suppressor gene.
XX
KW Modified retinoblastoma tumour suppressor; Rb protein; cancer therapy;
cellular proliferation inhibitor; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 7..2562
FT /start= a
XX
DN W09837091-A2.
XX
PD 27-AUG-1998.
XX
PE 19-FEB-1998; 98W0-USG3041.
XX
PR 20-FEB-1997; 97US 0048119.
XX
PA (BAYLOR) BAYLOR COLLEGE MEDICINE.
PA (TEXAS) UNIV TEXAS SYSTEM.
XX
PI Henedict WF, Hu S, Xu H, Zhou Y;
XX
WP1: 1998-480788/41.
XX
P-PSDB: AAV69367.
XX
PT Retinoblastoma suppressor protein with N-terminal modification
inhibiting cellular proliferation, particularly cancer
XX
PS claim 22; page 158 162; 249pp; BioTish.
XX
CC This sequence encodes a modified retinoblastoma tumour suppressor
protein (RbSP) of the invention. The proteins can be used for inhibition
of cellular proliferation, when coadministered with a p53 protein. The RbSPs
can be used for treating diseases characterised by abnormal cellular
proliferation, particularly cancers. The RbSPs have a broader spectrum of
activity than wild type RbSPs.
SQ Sequence 3323 bp; 1114 A; 605 C; 591 G; 1013 T; 0 other;
Query Match 99.78; Score 4257; 198 19; Length 3423;

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GenPro version 5.1.3
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XX W98-0391-A2.
 XX 27 APR-1998.
 XX 19-FEB-1998; 98W0-US03041.
 XX 20-FEB-1997; 9705-0038118.
 XX (RAY) Saylor College Medicine.
 XX (TEXA) Univ Texas System.
 XX Benedit WF, Hu S, Xu H. *Proc Natl Acad Sci USA* 99:1111-1116 (2002).
 XX WB: 1998-480788/41.
 XX PFSUB: AAW69367.
 XX Retinoblastoma suppressor protein with N-terminal modification -
 XX inhibiting cellular proliferation, particularly cancer
 XX Claim 22, Page 158-162, 349pp, English.
 XX This sequence encodes a modified retinoblastoma tumor suppressor
 XX protein (RTSP) of the invention. The proteins can be used for inhibiting
 XX cellular proliferation when coadministered with a p53 protein. The p53ps
 XX can be used for treating diseases characterized by abnormal cellular
 XX proliferation, particularly cancers. The RTSPs have a broader spectrum of
 XX activity than wild type RTSPs.
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 RESULT 15
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 AC AAA29391;
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 DT 12-SEP-2000 (first entry)
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 DE Human retinoblastoma gene.
 XX
 KW hEST2, telomerase, catalytic subunit, reverse transcriptase; life-span;
 KW retinoblastoma; p53; tumour suppressor; inhibitor of telomerase;
 KW proliferation; immortal; tumour therapy; macular degeneration; activator;
 KW INK4, ss.
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 OS Homo sapiens.
 XX
 PN W0200031238 A2.
 XX
 DB 02-JUN-2000.
 XX
 AP 24-NOV-1999; 99W0-US27907.
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 PP 25-NOV-1998; 98US-0109891.
 PP 17-FEB-1999; 99US-0120549.
 XX
 PA (GENE-) GENETICA INC.
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 PI Hannon GJ, Beach D;
 DR WPI: 2000-400055/34.
 XX
 PR New method for increasing the proliferative capacity of cell lines
 PR by co-transfected agents reversibly activating telomerase
 PI activity and re-sensitizing cells to p53 and pRb pathways useful
 in treating age related diseases

XX claim 5, Page 121-123; 12:49:10 British.

XX The invention concerns methods and reagents for extending the life-span, e.g. the number of mitotic divisions, of a cell. The method relies on activation of a telomerase activity and inhibition of one or both of a retinoblastoma (Rb)/INK4 pathway or a p53 pathway. Phosphorylation of Rb by cyclin dependent kinases, e.g.4 and cdk6, releases the cells into the division cycle. Binding of INK4 family members, e.g. the tumour suppressor p16INK4a, inhibits kinase activity, and results in growth arrest. Rb inactivators can selectively and reversibly inactivate an Rb/INK4 pathway, especially 4p16/p16INK4a pathway. The oncoprotein MDM2 is a cellular inhibitor of Rb/p16 function and the p53 tumour suppressor can also be used in the methods. Other molecules which can be used include cdk4 or cdk6 mutants. In particular, a cdk4 mutant is one which differs from at one or more of residues K22, p24, p26 and/or p67. Additional constructs include a papilloma virus E7 protein, or other viral oncoprotein which bypasses Rb and/or p53. Antisense constructs of the Rb and p16INK4a genes may also be used. The methods are useful for increasing the proliferative capacity of cells. The cells are subsequently of use in pharmaceutical and cosmetic preparations used to treat conditions related to (premature) ageing, e.g. macular degeneration and arteriosclerosis. The cells can also be used to replace tumour cell lines in vitro and for studies on biochemical and physiological aspects of growth and differentiation. Long lived (immortal) cells could also be of use in the production of normal or genetically engineered biotechnological products.

XX SQ Sequence 4839 BP; 1534 A; 902 C; 880 G; 1524 T; 0 other;

Alignment Scores:

Prod. No.: 0 Length: 4839
Score: 4467.60 Matches: 850
Percent Similarity: 173.27% Subtotal: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 99.84% Indels: 0
Gaps: 21

US 09 026 459A 33 (1-651) x AAAA29491 (1-4839)

QY 2 GluLysValSerSerValAspGlyValLeuGlyValTyrTriedGlyLysLysGluLeu 21
DB 472 GACAAAGGTTTCAATGCTGAGGAGATTCGACAGGTTAATTCACAAACCAAAAGGCAAC 431
QY 22 TrrpGlyTrrpCysLrrpPheLrrpAlaValAspLeuAspGluMetSerPheThrPheThr 41
DB 432 TGGAGAACTGTGATTTTATTTAGCACTGACCTAGAGATGATGATGATGATGATGATGAT 491
QY 42 GluLeuGlnTyrAsnGlnTrrpGlnTrrpSerValHisLysPhePheAsnLeuLeuLysGlnTrrp 61
DB 492 GAGGTACAGAAAGAAATAGCAAAATAGTGTGATTAATTTCTTAATTAATTAATTAATTAAT 551
QY 62 AspThrSerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysLysTyrAspValLeu 81
DB 552 GAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 611
QY 82 PheAlaLeuPheSerLysLeuLeuArgThrCysGlnLeuLeuTyrLeuThrGluProSer 101
DB 612 TTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 671
QY 102 SerSerThrSerThrGlnTrrpAsnSerAlaLeuValLeuLysValSerTrpTrpThrPhe 121
DB 672 AGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 731
QY 122 LeuLeuAlaLysGlyValValLeuGlnMetGluAspAspLeuValHisSerPheGlnLeu 141
DB 732 TTATAGCTAAAGGCAAAATATTAACAAATGGAAGATGATGATGATGATGATGATGATGATG 791
QY 142 MetLeuCysValLeuAspTyrPheHisLysLeuSerProProMetLeuLeuLysGluPro 161
DB 792 AGTGTAGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 851
QY 162 TrrpLysThrAlaValTrrpGlnTrrpTrrpTrrpTrrpTrrpTrrpTrrpTrrpTrrpTrrp 181

DB 852 TATAAACACAGCGCTTATACCAATTAATGAGTTCACCTGCAATACCAATACCAATACCAAT 911
QY 182 ArgSerAlaValLeuValLysGlnTrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrp 201
DB 912 AGCAGTGGACGAGTAAAGTAAATTAATGAGTTCACCTGCAATACCAATACCAATACCAAT 971
QY 202 TrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrp 221
DB 972 AAAGAAATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1001
QY 222 PheMetAsnSerLeuSerLeuValHisSerAspGlnTrrpGlnTrrpGlnTrrpGlnTrrp 241
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QY 242 TrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrp 261
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QY 262 HisAspGlnTrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrp 281
DB 1152 CATGATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAAT 1211
QY 282 TrrpSerAsnTrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrp 301
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DB 1272 ATCAACACATATCAACAAATATCAATGATGATGATGATGATGATGATGATGATGATGAT 1331
QY 322 AsnLeuTrrpSerTrrpPheAsnAspGlnTrrpValAsnTrrpGlnTrrpGlnTrrpGlnTrrp 341
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DB 1452 GTCAAGGATATAGGATATATCTTAAACAGAAATGCTGCTGCTGCTGCTGCTGCTGCTG 1511
QY 382 SerMetLeuTrrpSerTrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrp 401
DB 1512 TCAATGCTTAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAATAGAAAT 1571
QY 402 AspAsnTrrpPheHisMetSerLeuLeuAlaCysAlaLeuGlnValValMetAlaThrTrrp 421
DB 1572 GATCAACATTTTCAATGCTTATTTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1631
QY 422 SerArgSerThrSerGlnAsnLeuAspSerGlnTrrpAspLeuSerPheProTrrpLeuLeu 441
DB 1632 ACCAAGATACATCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1691
QY 442 AsnValLeuAsnTrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrpGlnTrrpGln 461
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DB 1752 GAAGGCAATTCACCAAGATCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1811
QY 482 GluSerLeuAlaTrrpLeuSerAspSerProLeuPheAspLeuTrrpLysGlnTrrpLysAsp 501
DB 1812 GAATGCTTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1871
QY 502 ArgGlnTrrpProThrAspHisLeuSerAlaCysPheLeuAsnTrrpGlnTrrpGlnTrrp 521
DB 1872 CAGAGAGAGGCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1931
QY 522 AsnHisThrAlaAlaAspMetTrrpLeuSerProValArgTrrpLysTrrpLysGlnTrrp 541

Genware version 5.1.3
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M nucleic nucleic search, using sw model

Run on: January 16, 2003, 15:29:17 : Search time 427.947 Seconds
(without alignments)
17531.794 Million cell updates/seq

Title: US 09 026 459A 42

Perfect score: 3424

Sequence: 1 GCGAATGACGAGAAAGTTC.....AAATGACGATATATCATATCAT 3323

Scoring table: IDENTITY NUC

Gapop 10.0, Gapext 1.0

Searches: 218526 seqs, 112599459 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum hit seq length: 6

Maximum hit seq length: 2000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

| Database : | | | | N.Geneset, 101002.* | | | |
|------------|--------|-------|--------|---------------------|-------------|-------|-------------------------|
| Result No. | Score | Match | Length | Hit | Description | Score | Description |
| 1 | 3424 | 100.0 | 3424 | 19 | AAV58443 | | Modified retinoblastoma |
| 2 | 3415 | 99.8 | 3392 | 19 | AAV58442 | | Modified retinoblastoma |
| 3 | 3415 | 99.8 | 3455 | 19 | AAV58441 | | Modified retinoblastoma |
| 4 | 3415 | 99.8 | 3555 | 19 | AAV58440 | | Modified retinoblastoma |
| 5 | 3415 | 99.8 | 3555 | 19 | AAV54990 | | DNA sequence of th |
| 6 | 3415 | 99.8 | 4839 | 21 | AAZ29391 | | Human retinoblastoma |
| 7 | 3415 | 99.8 | 4839 | 21 | AAZ88444 | | Human androgen rec |
| 8 | 3415 | 99.8 | 4839 | 24 | AAZ82874 | | Breast cancer rela |
| 9 | 3413.4 | 99.7 | 4597 | 15 | AAQ70536 | | Human retinoblastoma |

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Match | Length | Hit | Description |
|------------|--------|-------|--------|-----|-------------|
| 1 | 3424 | 100.0 | 3424 | 19 | AAV58443 |
| 2 | 3415 | 99.8 | 3392 | 19 | AAV58442 |
| 3 | 3415 | 99.8 | 3455 | 19 | AAV58441 |
| 4 | 3415 | 99.8 | 3555 | 19 | AAV58440 |
| 5 | 3415 | 99.8 | 3555 | 19 | AAV54990 |
| 6 | 3415 | 99.8 | 4839 | 21 | AAZ29391 |
| 7 | 3415 | 99.8 | 4839 | 21 | AAZ88444 |
| 8 | 3415 | 99.8 | 4839 | 24 | AAZ82874 |
| 9 | 3413.4 | 99.7 | 4597 | 15 | AAQ70536 |

| | | | | | | |
|----|--------|------|-------|----|----------|--------------------------------|
| 10 | 3313.4 | 99.7 | 4597 | 20 | AAQ44501 | Human retinoblastoma |
| 11 | 3311.8 | 99.7 | 3554 | 19 | AAV58452 | Modified retinoblastoma |
| 12 | 3311.8 | 99.7 | 4597 | 9 | AAV58459 | Human retinoblastoma |
| 13 | 3280.8 | 98.7 | 4740 | 24 | AAZ88444 | Modified retinoblastoma |
| 14 | 3257.4 | 98.0 | 3266 | 19 | AAV58444 | Protein for retinoblastoma |
| 15 | 3237.4 | 97.4 | 4579 | 9 | AAV58451 | Modified retinoblastoma |
| 16 | 3225.6 | 97.1 | 3323 | 19 | AAV58446 | Modified retinoblastoma |
| 17 | 3225.4 | 97.1 | 3461 | 19 | AAV58447 | Modified retinoblastoma |
| 18 | 3212.4 | 96.7 | 4218 | 19 | AAV54991 | DNA sequence of th |
| 19 | 3211.4 | 96.6 | 4243 | 15 | AAQ74900 | Retinoblastoma 94k |
| 20 | 3107 | 93.5 | 4113 | 19 | AAV58445 | Modified retinoblastoma |
| 21 | 3006 | 90.5 | 3347 | 19 | AAV58448 | Modified retinoblastoma |
| 22 | 2956.6 | 89.0 | 3383 | 19 | AAV58451 | Modified retinoblastoma |
| 23 | 2945.2 | 88.6 | 5056 | 10 | AAV58449 | cDNA of human retinoblastoma |
| 24 | 2944.6 | 88.6 | 5377 | 19 | AAV58450 | Modified retinoblastoma |
| 25 | 2827.4 | 85.1 | 3161 | 19 | AAV58449 | Modified retinoblastoma |
| 26 | 2623 | 78.9 | 2994 | 11 | AAQ44714 | Cancer suppressor |
| 27 | 2623 | 78.9 | 2994 | 14 | AAQ41545 | Retinoblastoma gene |
| 28 | 2623 | 78.9 | 2994 | 19 | AAV58448 | Retinoblastoma protein |
| 29 | 2623 | 78.9 | 2994 | 21 | AAZ15287 | Wild type human retinoblastoma |
| 30 | 2620 | 78.8 | 2995 | 20 | AAV58450 | Human p110 RB retinoblastoma |
| 31 | 2620 | 78.8 | 2995 | 20 | AAV58450 | cDNA encoding a retinoblastoma |
| 32 | 2620 | 78.8 | 2995 | 22 | AAV58450 | Retinoblastoma tum |
| 33 | 2620 | 78.8 | 2995 | 22 | AAV58450 | Retinoblastoma tum |
| 34 | 2620 | 78.8 | 2995 | 23 | AAV58450 | Retinoblastoma tum |
| 35 | 2618.4 | 78.8 | 2995 | 16 | AAQ86498 | Retinoblastoma tum |
| 36 | 2613.6 | 78.7 | 2995 | 16 | AAQ86498 | Human Rb110 cDNA |
| 37 | 835 | 25.1 | 18304 | 20 | AAV58450 | Human retinoblastoma |
| 38 | 831.8 | 25.0 | 18177 | 10 | AAV58450 | DNA of human retinoblastoma |
| 39 | 220.8 | 6.6 | 1698 | 18 | AAV58450 | Antisense sequence |
| 40 | 220.8 | 6.6 | 1802 | 18 | AAV58450 | Correct tandem repeat |
| 41 | 220.8 | 6.6 | 2734 | 18 | AAV58450 | Construct PMK12/AS |
| 42 | 220.8 | 6.6 | 3455 | 18 | AAV58450 | Construct PMK12/AS |
| 43 | 220.8 | 6.6 | 4743 | 18 | AAV58450 | Construct PMK12/AS |
| 44 | 218.8 | 6.6 | 909 | 16 | AAV58450 | Retinoblastoma protein |
| 45 | 218.8 | 6.6 | 1697 | 16 | AAV58450 | Retinoblastoma protein |

ALIGNMENTS

| | |
|----------|---|
| RES001 1 | |
| AAV58443 | |
| 19 | AAV58443 standard. DNA. 3423 bp. |
| XX | |
| AC | AAV58443; |
| XX | |
| 10 | 02-DEC-1998 (first entry) |
| XX | |
| 10 | Modified retinoblastoma tumour suppressor gene. |
| XX | |
| 10 | Modified retinoblastoma tumour suppressor. Also protein cancer therapy. |
| XX | |
| 10 | Cellular protein cancer inhibitor. |
| XX | |
| 10 | Homo sapiens. |
| XX | |
| 10 | Key |
| XX | |
| 10 | Location/Qualifiers |
| XX | |
| 10 | 7.12562 |
| XX | |
| 10 | /tag- a |
| XX | |
| 10 | W0837091 A2. |
| XX | |
| 10 | 27-AUG-1998. |
| XX | |
| 10 | 19-FEB-1998; 98W0-US03041. |
| XX | |
| 10 | 20-FEB-1997; 97US-0048118. |
| XX | |
| 10 | (BAYU) BAYLOR COLLEGE MEDICINE. |
| XX | |
| 10 | (TEXA) UNIV TEXAS SYSTEM. |
| XX | |
| 10 | Benedict WF, Hu S, Xu H, Zhou Y. |
| XX | |

XX
Sequence 3092 BP: 1137 A; 614 C; 607 G; 1034 T; 0 other;

[illegible][illegible]


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DB 2421 ATTCGGAATTCGACAAAGTTCGACAAATTAATACAGATGCTATGTAACAGTCAGCGGCTG 2480
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DB 3321 TATTCGAATCAATCAAGGAAGTAAAGCTCTTAACATCTGAATAAAAGTATAGCTTTGA 3380
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DB 3381 TATTCGAATCAATCAAGGAAGTAAAGCTCTTAACATCTGAATAAAAGTATAGCTTTGA 3440
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AAV58440
10 AAV58440 standard; DNA; 4555 bp.
XX
AC AAV58440;
XX
02-DEC-1998 (first entry)
XX
Modified retinoblastoma tumour suppressor gene.
XX
Modified retinoblastoma tumour suppressor; RBP protein; cancer therapy;
XX
cellular proliferation inhibitor; ss.
XX
Homo sapiens.
XX
Key Location/Qualifiers
CDS 7..2794
/*aa- a
XX
W09847091-A2.
XX
27-AUG-1998.
XX
19-FEB-1998; 98W0-0503041.
XX
20-FEB-1997; 97US 0038118.
XX
(BAYLOR COLLEGE MEDICINE.
PA (TEXAS) UNIV TEXAS SYSTEM.
XX
Renedit WF, Hu S, Xu H, Zhou Y;
XX
WPI; 1998-480786/41.
DR
P-PSDB; AAV69464.
XX
Retinoblastoma suppressor protein with N terminal modification
inhibiting cellular proliferation, particularly cancer
XX
Discourse; Page 121-126; 249pp; English.
XX
This sequence encodes a modified retinoblastoma tumour suppressor
protein (RBP) of the invention. The proteins can be used for inhibiting
cellular proliferation, when coadministered with a p53 protein. The RBP
can be used for treating diseases characterized by abnormal cellular
proliferation, particularly cancers. The RBP have a broader spectrum of
activity than wild type RBPs.
XX
Sequence 4555 bp; 1171 A; 684 C; 653 G; 1047 T; 0 other;
SQ

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Query Match 99.88; Score 4415; DB 19; Length 4555;
Rest Local Similarity 100.00; Pval. No. 0;
Matches 3315; Conservative 0; Mismatches 0; Labels 0; Gaps 0;
QY 9 GGAGAAATTTTCATCTGTGATGGAGTATGGAGTATATATTTTCAAAAGGAAAT 68
DB 240 GGAGAAATTTTCATCTGTGATGGAGTATGGAGTATATATTTTCAAAAGGAAAT 249
QY 69 GTGGGAAATCTGTATCTTTATGTAGTATGATGATGATGATGATGATGATGAT 128
DB 300 GTGGGAAATCTGTATCTTTATGTAGTATGATGATGATGATGATGATGATGAT 359
QY 129 TGAGTATGAGAAATACAGAAATACAGTATGATGATGATGATGATGATGATGAT 188
DB 360 TGAGTATGAGAAATACAGAAATACAGTATGATGATGATGATGATGATGATGAT 419
QY 189 TGATAGCAGTATGAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 248
DB 420 TGATAGCAGTATGAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 479
QY 249 GTTTCGATCTTCAGTAAATGGAGAAATGATGATGATGATGATGATGATGATGAT 508
DB 480 GTTTCGATCTTCAGTAAATGGAGAAATGATGATGATGATGATGATGATGATGAT 549
QY 309 CAGTTCGATATCTACGAAATACAGTATGATGATGATGATGATGATGATGATGAT 368

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DB 234 GCAGAAATTCATCTGTCGAGGATATGGGAGGTATATTCACAAAGAAAAGGAAC 293
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QY 309 TGAATACAGAAAACATACAAATACAGTTCATTAATTTTAACTTACTTAAAGAAAT 468
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QY 369 TGAATACAGAAAACATACAAATACAGTTCATTAATTTTAACTTACTTAAAGAAAT 428
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DB 1316 ATCCATGCTTAAATACAGAAAGAACGATATATCAATCAAAAATTTAGCAAAATTTTGA 1433
QY 1209 TCAAAATATTTTCAATGCTTATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1368
DB 1210 TCAAAATATTTTCAATGCTTATTTTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1493
QY 1259 TAGGAGAGTACATCTGAGAACTGATCTGAGAAAGATTTTGTCTTCTGCTGCTGCTGCTG 1428
DB 1260 TAGGAGAGTACATCTGAGAACTGATCTGAGAAAGATTTTGTCTTCTGCTGCTGCTGCTG 1553
QY 1329 GAATGCTTAAATTAAGAACTTTGATTTTAAAGATGATGAAAGATTTTATCAAGG 1488
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QY 1389 AGAAGGCACTTGCACAGAGAAATGATTAAGAACTTTTGAAGAGATGCTGCTGCTGCTGCTG 1448
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DB 1510 CGGAGAGAGAGAACTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1793
QY 1569 TAAATACAGTTCAGGATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1528
DB 1570 TAAATACAGTTCAGGATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1853
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DB 1630 TAAATACAGTTCAGGATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1913
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QY 1929 TAAATACAGTTCAGGATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1988
DB 1930 TAAATACAGTTCAGGATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2213
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QY 2109 TAAATACAGTTCAGGATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2168
DB 2110 TAAATACAGTTCAGGATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2393
QY 2169 TAAATACAGTTCAGGATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2228
DB 2170 TAAATACAGTTCAGGATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2453

XX W09847091 A2.
 XX 10 AUG-1998.
 XX 19 FEB-1998: 98W0-0503041.
 XX 20 FEB-1997: 97DS 0038118.
 XX (HAY)) HAYLOR COLLEGE MEDICINE.
 XX (LISA) UNIV TEXAS SYSTEM.
 XX Benedict WF, Hu S, Xu H, Zhou Y.
 XX W011998-480788/41.
 XX P 1998: AAW69366.
 PT Retinoblastoma suppressor protein with N-terminal modification -
 PT inhibiting cellular proliferation, particularly cancer
 XX (Date: 22; Page 150-155; 240pp; English
 XX this sequence encodes a modified retinoblastoma tumour suppressor
 XX protein (RTPSP) of the invention. The proteins can be used for inhibiting
 XX cellular proliferation, when coadministered with a p53 protein. The RTPSPs
 XX can be used for treating diseases characterised by abnormal cellular
 XX proliferation, particularly cancers. The RTPSPs have a broader spectrum of
 XX activity than wild type RbSPs.
 XX Seq-Info: 492 BP; 1147 A; 614 C; 607 G; 1034 T; 0 other;
 Seq-Id: 26-459a-31 (1-874) x AAW58442 (1-3392)
 Alignment Statistics:
 Pred. No.: 0 Length: 3392
 Score: 4504.00 Matches: 874
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 19 Gaps: 0
 05 09 026-459a-31 (1-874) x AAW58442 (1-3392)
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 DB 7 ATGAGTTTACTGCTATTATGTCAGCAATTAAGACATACATCATGCTACAGACAGACACT 66
 QY 20 TrpLeuThrTrpGluLysValSerSerValAspGlyValLeuGlyCyllyrIleGlnLys 40
 DB 67 TGGTAACTTGGGAGAAATTTATCTGATGATGAGAGTATGAGAGTATATATATCAAAAG 126
 QY 41 LysLysIleLeuTrpGlyIleGlyCyllePheIleAlaAlaValAspLeuAspGluMetSer 60
 DB 127 AAAAAAGAACTGGGAGAAATTTATGATGATGAGAGTATGAGAGTATATATATCAAAAG 186
 QY 81 PheThrThrThrGluLeuGluLysAsnIleGluIleSerValIleLysPheAsnLeu 80
 DB 167 TTTATTTTACTGAGATACAGAAACATAGAAATCAGTGTCCATATATTTTAACTTA 246
 QY 81 LeuLysGluIleAspThrSerThrLysValAspAsnAlaMetSerArgLeuLeuLysLys 100
 DB 247 GTAAAAAAATTTAT 406
 QY 101 TyrAspValLeuPheAlaLeuPheSerLysLysGluArgThrGlyGluLeuIleTyrLeu 120
 DB 307 TATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 366
 QY 121 ThrGlnProSerSerIleSerThrGluIleAsnSerAlaLeuValLeuLysValSer 140
 DB 467 AT 426
 QY 141 TrpIleThrPheLeuLeuAlaLysGlyGluValGluMetGluAspLeuValIle 160
 DB 427 TGGAT 486

QY 161 SerPheGluLeuMetLeuGlyValLeuAspTyrPheIleLysLeuSerProMetLeu 180
 DB 487 TCAATTCAGTTAAATGCTATGCTGCTTACATATTTTAAACATGCTACCTGCTCAATG 546
 QY 181 LeuLysGlyIleThrLysThrAlaValIleThrLeuLeuAsnGlySerProArgThrProArg 200
 DB 547 CTCAAAGAACCATATAAAGACGCTGTTATACCATTAATGGTTCATCTGGAAATACACAG 606
 QY 201 ArgGlyGlnAsnArgSerAlaMetIleAlaLysGlnLeuGluAsnAspThrArgIleIle 220
 DB 607 CCAGGTACAGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 666
 QY 221 GluValLeuGlyLysLysLysLysLysLysLysLysLysLysLysLysLysLysLys 240
 DB 667 GAACCTTCCTTAAAGAACATCAATCTAAATATATACATCAGCTCAAAAATGCTTAT 726
 QY 241 AsnPheIleThrPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuThrGluVal 260
 DB 727 AATTTATACCTTTTATGAAATCTCTTGAGCTTGTAACTATCAATCTAAATCTCAAGGTT 786
 QY 261 GluAsnLeuSerLysSerLysGlyGluIleIleIleLysLysLysLysLysLysLys 280
 DB 787 GAAATCTCTTCAAAGCATACGAAGAAATTTATCTTAAAAATTAACATCTACATCAACA 846
 QY 281 LeuPheLeuAspHisSerLysThrLeuGlnThrAlaSerIleAspSerPheGluThrGln 900
 DB 847 TTATTTTGGATCATCAATAAAACTCTTCAGACTGATCTATACACAGCTTTTCAAAACACAG 906
 QY 301 ArgThrProArgLysSerAsnLeuAspGluGluValAsnValIleProProHisThrPro 320
 DB 907 AGAACACACAGAAAAATTAACCTTGATGAGAGGTAAATGTAATCTCTCCACATCTCCA 966
 QY 321 ValArgThrValMetAsnThrIleGlnGlnGlnMetIleLeuAsnSerAlaSerAsp 340
 DB 967 GTTAGGACCTGTATGACACACTATCCACAAATTAATGATCATTTTAAATTCACCAAC 1026
 QY 341 GluProSerGluAsnLeuIleSerTyrPheAsnAsnGlyThrValAsnProLysLysSer 360
 DB 1027 CAACCTTCAGAAATCTGATTTCTTATTTTAAACATGACACAGTGAATCCAAAAGAAAG 1086
 QY 361 LeuLeuLysArgValLysAspIleCyllyrIlePheLysGlyLysPheAlaLysAlaVal 380
 DB 1087 ATACTGAAAGACGTGAAGCATATATATATATATATATATATATATATATATATATAT 1146
 QY 381 GlyClnGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgIleCyllyr 400
 DB 1147 GGACAGGCTTGTGTCGAAATGGATGACAGCAGATCAAACTTGGAGTTGCGCTGCTAT 1206
 QY 401 ArgValMetGluSerMetLeuLysSerGluGluArgLeuSerIleGluAspPheSer 420
 DB 1207 CCAGTAATGCAATCCCAAGCTTAAATCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1266
 QY 421 LysLeuLeuAsnAspAsnIlePheHisMetSerIleLeuAlaGlyAlaLeuGluVal 440
 DB 1267 AATCTTGAAATGAAAT 1326
 QY 441 MetAlaThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPhe 460
 DB 1327 ATGCCACATATAGCAGAGAGTACATCTCAGAACTCTTCAATCTGGAACACAGATCTGCT 1386
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 QY 481 PheLysAlaGluGlyAsnLeuThrArgIleGlnMetIleLysHisLeuGluArgTyrSer 500
 DB 1447 TTTATCAAGACAG 1506
 QY 501 HisArgIleMetGluSerLeuAlaThrLeuSerAspSerProLeuPheAspLeuLys 520
 DB 1507 CATCGAATCATGAAATCCCTTGCATGCGCTCTCAGATCTACCTTTATTCATCTTAT 1566
 QY 521 GluSerLysAspArgIleGlyProThrAspHisLeuGluSerAlaGlyProLeuAsnLeu 540


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47 342  ProSerGluAsnGluSerThrPheAsnAsnCysThrValAsnProLysGluSerIle 361
1b 344  CTTTCAGAAATGCGATTCCTATTATTCATGTCAGTGAATGCAAGAAAGATATA 1383
47 362  LeuLysArgValLysAspIleCysTyrIlePheCysCysLysPheAlaLysAlaValGly 381
1b 364  CTGAAACAGTGAAGGATAAGGATAAGGATAAGGATAAGGATAAGGATAAGGATA 1443
47 382  GluLysValGluIleLeuLysGluArgTyrLysLeuGlyValArgLeuTyrTyrArg 401
1b 384  TACGGTCTCTGCTGAAATTCGATACACACGATACAAATTCGAGTTCGCTGATAC 1503
47 402  ValMetGluSerMetLeuLysSerGluGluLysIleGluAsnProLys 421
1b 404  GTATGCAATCATGCTTAAATTCAGAGAGAGAGATATCCATTCAAAATTTTACAAA 1563
47 422  LeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValMet 441
1b 424  CTTCGATGACAAATCTTCATATGCTTATATGCTTATATGCTTATATGCTTATAT 1623
47 442  AlaThrTyrSerArgSerThrSerGluAsnSerCysLeuThrAspLeuSerPhePro 461
1b 444  GTCATATATAGCAGAGATACATGCAATCTTCATGCTGGAACAGATTTGCTTCCCA 1683
47 462  TrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleCysSerPhe 481
1b 464  TGAATCTGATGCTTAAATTTAAAGGCTTTGATTTTACAAAGTATGCAAGATTTT 1743
47 482  IleLysAlaGluLysLeuAsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHis 501
1b 484  ATCAAACTCAGAAATCACTTCACACAGAGAAATGATATGAAATTTTGAAGCATCT 1803
47 502  ArgIleLeuGluSerLeuAlaTyrLeuSerAspSerProLeuPheAspLeuLeuLysLeu 521
1b 504  GAAATCAAGAAATCTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1863
47 522  SerLysAspArgGluGlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuPro 541
1b 524  TCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1923
47 542  LeuGluAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLys 561
1b 544  CTACAGATAATATACATGATATATATATATATATATATATATATATATATATAT 1983
47 562  LysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAla 581
1b 564  AAAGTCTTAAATATAGGCTGATAATATATATATATATATATATATATATATATAT 2043
47 582  PheGlnThrGluLysProLeuLysSerThrSerGluSerLeuPheCysTyrLysValTyr 601
1b 584  TTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2103
47 602  ArgLeuAlaTyrLeuArgAlaAsnThrLeuCysGluArgLeuLeuSerGluHisProGlu 621
1b 604  GAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2163
47 622  LeuGluHisIleIleThrThrLeuPheGlnHisThrLeuLeuAsnGluTyrGluLeuMet 641
1b 624  TACAGATAATATATATATATATATATATATATATATATATATATATATATATAT 2223
47 642  ArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrCysIleCysLysValLys 661
1b 644  AAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2283
47 662  AsnIleAspLeuLysPheCysIleIleValThrAlaTyrLysAspLeuProHisAlaVal 681
1b 664  AATATACACCTTAATATCAAAATCATATACAGCATACAGCATACAGCATACAGCAT 2343
47 682  GlnGlnThrPheLysArgValLeuIleLysGluGluGlyTyrAspSerIleLeuValPhe 701
1b 684  TACAGAGATATCAACGCTGCTTCAATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2403

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47 702  TyrAsnSerValPheMetGluArgLeuGlySerThrAsnIleLeuGluClnIlyTyrAlaSerIle 721
1b 704  TATACTCGCTCTTCATGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 741
47 722  ProProThrLeuSerProIleProHisIleProArgSerProTyrLysPheProSerSer 741
1b 724  GCGCTTACCTTTGTCACCAATACCTACATACCTACCAAGAGAGAGAGAGAGAGAG 752
47 742  ProLeuArgIleProGlyLysAsnIleTyrIleSerProLeuLysSerProTyrLysIle 761
1b 744  CCGTTAGAGATTCGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 768
47 762  SerGluGlyLeuProThrProHisMetThrProArgSerArgIleLeuValSerIle 781
1b 764  TCAGAGAGCTTTCGACACATACCAAAATGATTCGAGATCAGAGATCTTATATATAT 784
47 782  GlyGluSerPheGlyThrSerGluLysPheGluLysIleAsnGluMetValCysAsnSer 801
1b 784  CAGCTGCTGCTTAAAAAATATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 792
47 802  AsnArgValLeuLysArgSerAlaGluGlySerAspProIleLysLeuLysLeuLys 821
1b 804  CAGCTGCTGCTTAAAAAATATTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 796
47 822  ArgPheAspIleCysGlySerAspGluAlaAspGlySerLysHisLeuProGlyGluSer 841
1b 824  CCGTTTCATATTCAGAGATATCAAAATGATTCGAGATCAGAGATCTTATATATAT 823
47 842  LysPheGluGlnLysLeuAlaGluMetThrSerThrArgMetGluLysGluLys 861
1b 844  AAATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 863
47 862  MetAsnAspSerMetAspThrSerAsnLysGluLysLys 874
1b 864  ATGATATATATATATATATATATATATATATATATATATATATATATATATAT 872

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RESULT 4
 AAV40004
 ID AAV40004 standard; DNA; 2994 BP.
 XX
 AC AAV40004;
 XX
 DI 15 FEB-1999 (first entry)
 XX
 DE Retinoblastoma protein RB.
 XX
 KW Retinoblastoma protein RB; E2F; transcription factor; human;
 KW bladder cancer; rhabdomyosarcoma; angiosarcoma; diabetic retinopathy;
 KW thyroid hyperplasia; Crave's disease; psoriasis;
 KW benign prostatic hypertrophy; Li-Fraumeni syndrome;
 KW peripheral vascular disease; therapy; ss.
 XX
 OS Homo sapiens.
 XX
 KY Location/Qualifiers
 FI 149,1292
 FT /*aa= a
 XX
 PN W09821238-A1.
 XX
 IN 22-MAY-1998.
 XX
 PF 13 NOV 1997; 97NOV-0521821.
 XX
 PR 14-FEB-1997; 97FEB-0801092.
 XX
 PR 15-NOV-1996; 96NOV-0751517.
 XX
 PA (CANU-) CANU1 INC.
 XX
 PI Anita Lam D, Gregory RJ, Wells KN.
 XX
 IN WP1: 1998-297858/26.
 XX
 IN P-PSDB; AAW62465.

10 424 AACCAACCTGCGGAAATGCGATGATGATGACCTAGACATGACATGCTGCTC 483
 20 62 ThrProThrGluAlaGlnLysAsnGluLeuSerValHisLysPhePheAsnLeu 81
 40 464 ATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 543
 60 92 LysGluThrAspLysThrLysValAspAsnAlaMetSerArgGlnGlnLysLys 101
 80 544 AAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 603
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 120 604 CAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 663
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 180 142 ThrThrPheGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 161
 200 724 AT 783
 220 162 PheLeuLeuMetLeuLysValLeuAspTyrPheLeuLysLeuSerProPheMetLeuLeu 181
 240 784 AT 843
 260 182 LysGluProTyrLysThrAlaValProLeuAsnGlySerProArgThrProArg 201
 280 844 AAAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 903
 300 202 GlyPheAsnArgSerAlaArgAlaLysLysLeuGlnAsnAspThrArgLeuGln 221
 320 904 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 963
 340 222 ValLeuGlyLysGlnLysLysLysLysLysLysLysLysLysLysLysLys 241
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 400 1024 TTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1083
 420 262 AsnLeuSerLysArgTyrGlnLeuLysLysLysLysLysLysLysLysLysLys 281
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 700 402 ValMetGlnSerMetLeuLysSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 421
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422 LeuLeuAsnAspSerLysLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 441
 1564 CTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1623
 442 AlaThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspSerPhePro 461
 1624 GGCATATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1683
 462 TrpPheLeuAsnValLeuAsnLeuLysAlaPheAspThrTyrLysValLeuLeuSerPhe 481
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 522 SerLysAspArgGlnLysProThrAspHisLeuLeuSerAlaLysProLeuAsnLeuPro 541
 1864 TCAAAAGGACGAGAGGCGATTCGATGATGATGATGATGATGATGATGATGATGATGAT 1923
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 1924 CTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1983
 562 LysGlySerThrArgArgValAsnSerThrAlaAsnArgLeuGlnGlnGlnGlnGln 581
 1984 AAAGGCTCAATACGCGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2043
 582 PheGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrLysValTyr 601
 2044 TCCGAGACCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2103
 602 ArgLeuAlaTyrLeuArgLeuAsnThrLeuLysGlnArgLeuLeuSerGlnHisProGlu 621
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 2584 TCAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2643

40 42 LeuThrThrPheLysValSerSerValAspGlyValLeuGlyValThrPheGluLysLys 41
41 44 AAAC1GGCAAAAGGAC 423
42 46 CysThrLeuThrPheGlyLeuLysLeuThrPheGluAlaValAspLeuAspGluMetSerPhe 61
43 48 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1563
44 44 AAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 483
45 46 ThrPheThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 81
46 48 AATTTTAC 543
47 82 LysThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLys 101
48 84 AAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 603
49 86 AsnValLeuPheAlaLeuPheSerLysLeuGluArgThrCysGluLeuLeuLeuLeuThr 121
50 88 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 663
51 122 ThrProSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSerSer 141
52 124 CAACCCAC 723
53 142 ThrPheLeuLeuAlaLysGlyValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 161
54 144 ATAC 783
55 162 PheGluLeuMetLeuCysValLeuAspThrPheThrLeuLeuLeuLeuLeuLeuLeu 181
56 164 ITTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 843
57 182 LysGluProLysThrAlaValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 201
58 184 AAAGAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 903
59 202 GlyGluAsnAspSerAlaThrAlaLysGlyLeuLeuLeuLeuLeuLeuLeuLeuLeu 221
60 204 GGCAC 963
61 222 ValLeuLysGlyLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 241
62 224 ATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1023
63 242 PheLeuProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuLeuLeuLeu 261
64 244 ATATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1083
65 262 AsnLeuSerLysArgThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 281
66 264 AATCTCTTCAAGGATCAAGGATCAAGGATCAAGGATCAAGGATCAAGGATCA 1143
67 282 PheLeuAspHisAspLysThrLeuGluThrAspSerThrLeuLeuLeuLeuLeuLeu 301
68 284 ATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1203
69 302 ThrProArgLysSerAsnLeuAspGluGluValAsnValLeuProPheHisThrProVal 321
70 304 ATACCAAGAAAGATCAAGGATCAAGGATCAAGGATCAAGGATCAAGGATCA 1263
71 322 ArgThrValMetAsnThrThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 341
72 324 AATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1323
73 342 ThrSerGluAsnLeuLeuSerThrPheAsnAsnCysThrValAsnProLysGluSerPhe 361
74 364 GTTACAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1383
75 382 ThrThrArgValThrAsnThrGlyThrThrPheCysGluLeuLeuLeuLeuLeuLeu 381
76 384 GACAAAGACATCAAGGATCAAGGATCAAGGATCAAGGATCAAGGATCAAGGATCA 1443
77 402 ThrThrCysValThrLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 401

1444 CAGGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 1504
402 ValMetGluSerMetLeuLysSerGluGluGluArgGluSerThrGluAsnPheSerLys 421
1504 GTAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 1564
422 LeuLeuAsnAspAspThrPheHisMetSerLeuLeuAlaCysAlaLeuGluValValMet 441
1564 CTTCTGAAATGCAACAAATTTTCAATAGTCTTATTTGGGTCGGGTCCTTCAAGGTC 1624
442 AlaThrThrSerArgSerThrSerGluAsnLeuAspSerGlyThrAspLeuSerPhePro 461
1624 GGCACATATAGCAGAGATACATCTCAGAACTTCTTATTTTACAAAGTCATGCAAGTTT 1744
462 ThrPheLeuAsnValLeuAsnLeuLysAlaPheAspPheThrLysValLeuGluSerPhe 481
1684 TGGATTTCTGAATGTCGTTAAATTTAAAGGCTTTATTTTACAAAGTCATGCAAGTTT 1744
482 ThrLysAlaGlyGlyGluLeuThrArgGluMetThrLysHisLeuGluArgCysGluHis 501
1744 ATCAAAATGCAAGGCTAACTTCAATAGCAAAATGCAAAATGCAAAATGCAAAATG 1804
502 ArgLeuMetGluSerLeuAlaThrPheSerAspSerPheLeuPheAlaLeuLeuLys 521
1804 GGAATCATGCAATGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCTTCAAGGCT 1864
522 SerLysAspArgGluLeuThrAspHisLeuGluSerAlaCysProLeuAsnLeuPro 543
1864 TCAAGACCGGAG 1924
542 LeuGluAsnAsnHisThrAlaAlaAspMetThrLeuSerProValArgSerProLysLys 561
1924 CTTCCAGAAATATCACACATGCTAGCAATATATATATATATATATATATATATAT 1984
562 LysGluSerThrThrArgValAsnSerThrAlaAlaGluGluThrGluAlaThrSerAla 581
1984 AAGGTTTAAATACGATGTAATTTCTTCAATGCAAGGCTTCAAGGCTTCAAGGCT 2044
582 PheGluThrGluLysThrLeuLysSerThrSerLeuSerPheThrLysValLeuLeu 601
2044 TTTCCAGACCAAG 2104
602 ArgLeuAlaThrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProHis 621
2104 GGGTATGCTATCTGGGCTAAATATATATATATATATATATATATATATATATATAT 2164
622 LeuGluHisThrLeuThrPheThrLeuPheThrLeuGluAsnGluThrGluLeuMet 641
2164 TTAGAACATATCATCTGACATCTTTTTCAGCAAGGCTTCAAGGCTTCAAGGCTTCA 2224
642 ArgAspArgHisLeuAspGluThrMetMetCysSerMetThrGlyThrCysLysValLys 661
2224 ACAGACAGGATTTGAGCAAAATATATATATATATATATATATATATATATATATAT 2284
662 AsnThrLeuLysPheLysThrLeuValThrAlaThrLysAspLeuProHisAlaVal 681
2284 AATATAGAGCTTAAATATCAAAATATATATATATATATATATATATATATATATAT 2344
682 GAGGLeuThrPheLysArgValLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 701
2444 CAGGCTATTTTAAATGCTTTTAAATGCTTTTAAATGCTTTTAAATGCTTTTAAATG 2404
702 ThrAsnSerValPheMetGluArgLeuLysThrAsnThrLeuGluThrAlaSerThrArg 721
2404 TATAATGCTTTTAAATGCTTTTAAATGCTTTTAAATGCTTTTAAATGCTTTTAAATG 2464
722 ThrProThrLeuSerPheLeuProHisThrLeuProArgSerProThrLysPheProSerSer 741
2464 CCCCCACCTTCTACCAATACCTTCTACCAATACCTTCTACCAATACCTTCTACCAAT 2524
742 ProLeuArgLeuProGlyAsnThrLeuSerProLeuLysSerProThrLysLeu 761

412 LeuLeuAspAspValLeuPheHisMetSerLeuLeuAlaCysAlaLeuGluValValMet 441
 413 1584 GTCAGAAAGACAAACATTTTCAATAGCTTTAATGGGCTGGCTCTTGAGGTTTGAAGC 1623
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 415 AlaThrTyrSerArgSerThrSerGluAsnLeuAspSerGlyThrAspLeuSerPhePro 461
 416 1624 GCAACATATACAGAGAGTACATCTGCAATCTTGATTTGAAAGATTTGTCTTTTTCGA 1683
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 418 ThrPheLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValLeuGluSerPhe 481
 419 1684 TGGATTTCGAATGCTGCTTAATTTTAAAGAGCTTTGATTTTACAAAGTGAATCAAGATTTT 1743
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 421 LeuLeuAlaLeuGlyAsnSerThrArgGluMetIleLysHisLeuGluArgGlyGluHis 501
 422 1744 ATCAAGACAGAAAGGAACTTACACAGACAAAGAAAGAAACATTTAGAACCATTTGGAACAT 1803
 423
 424 ArgIleMetGluSerLeuAlaTriPheSerAspSerProLeuPheAspLeuIleLysGln 521
 425 1804 GAATATGGAATGCTTGTGATGGCTCTGACATTCACGCTTTATTGTATCTTATTAAACAA 1863
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 427 SerGlySerArgGluGlyProIleHisAspHisLeuGluSerAlaCysProLeuAsnLeuPro 541
 428 1864 TCAAAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1923
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 430 LeuGluAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLys 561
 431 1924 GTCGACAAATAC 1983
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 433 LysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAla 581
 434 1984 AAAGGTCGAAATGAGCGGTAAATTCACGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2043
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 436 PheGlnThrGlnIleProLeuLysSerThrSerLeuSerLeuPheTyrLysValTyr 601
 437 2044 TTTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 2103
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 439 ArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGlu 621
 440 2104 GAGTACAGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2163
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 442 LeuLeuHisLeuLeuLeuThrLeuPheGluLeuLeuLeuLeuLeuLeuLeuLeuLeu 641
 443 2164 TTAGAACATATCATTTGAGACCTTTTTCAGCACATTTTTCAGCACATTTTTCAGCACATTT 2223
 444
 445 ArgAspArgHisLeuAspIleIleMetMetCysSerMetCysGlyIleCysLysValLys 661
 446 2224 AGAAGACAGCAATTTGCAAGCAATTTGCAAGCAATTTGCAAGCAATTTGCAAGCAATTTG 2283
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 448 AsnLeuAspLeuLysPheLysIleLeuValThrAlaTyrLysAspLeuProHisAlaVal 681
 449 2284 AATAATAGACCTTTAAATTTCAAAATCATTTGAAACACATACAGCAATTTGCAAGCAATTT 2343
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 451 GlnGlnThrPheLysArgValLeuLeuLysGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 701
 452 2344 CAAAGCAATTTTAAAGCAATTTTAAAGCAATTTTAAAGCAATTTTAAAGCAATTTTAA 2403
 453
 454 TyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGlnIleValAspThrArg 721
 455 2404 TAAATTCGAGCTTTATGATGAGAGCAATTTTAAAGCAATTTTAAAGCAATTTTAAAGCA 2463
 456
 457 ProProThrLeuSerPheTyrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 741
 458 2464 GAGGATATTTTAAAGCAATTTTAAAGCAATTTTAAAGCAATTTTAAAGCAATTTTAAAG 2523
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 460 ProLeuArgIleProGlyValLeuLeuLysSerProLeuLysSerProLeuLysSerPro 761
 461 2524 GATTAAGATATTTGAGAGGAAATTTTAAATTTTAAAGCAATTTTAAAGCAATTTTAAAG 2583
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 463 SerGlyGluLeuThrThrProThrLysMetThrProArgSerArgIleLeuValSerIle 781
 464 2584 TTAGAGGCTCTGCAAC 2643

QY 782 GlyLeuSerPheGlyThrSerGlyLysPheGlyLysIleAsnGlnMetValGlySerSer 801
 Db 2644 GTCAGAAAGACAAACATTTTCAATAGCTTTAATGGGCTGGCTCTTGAGGTTTGAAGC 2703
 QY 802 AspArgValLeuGlySerArgSerThrSerGluAsnLeuAspSerGlyThrAspLeuSer 821
 Db 2704 GCAACATATACAGAGAGTACATCTGCAATCTTGATTTGAAAGATTTGTCTTTTTCGA 2763
 QY 822 ArgPheAspIleGlnGlySerAspGlnAlaAspGlySerLysHisLeuProGlySerSer 841
 Db 2764 GCTTTTCATATTTGAAGCATCAGATGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 2823
 QY 842 LysPheGlnGlyLysLeuAlaGlnMetThrSerSerThrArgArgGlnGlnLysGlnLys 861
 Db 2824 AAATTTTCAACCAAACTGCGACCAAAATGACTTCTACTGCAACACAGCAAGCAAGCAAG 2883
 QY 862 MetAsnAspSerMetAspThrSerAsnLysGlnGluLys 874
 Db 2884 ATGAATATATATATGAT 2943
 RESULT 11
 AAV58441
 ID AAV58441 standard; DNA; 3455 BP.
 AC AAV58441:
 XX 02-DEC-1998 (first entry)
 XX Modified retinoblastoma tumour suppressor gene.
 XX Modified retinoblastoma tumour suppressor. Rb protein, cancer therapy;
 KW cellular proliferation inhibitor; ss.
 XX Homo sapiens.
 CS
 FH Key Location/Qualifiers
 FT CDS 7..2694
 FT /*tag- a
 XX W09837091-A2.
 XX 27 AUG-1998.
 XX 19-FEB-1998: 98W0-0503041.
 XX 20-FEB-1997: 97US-0038118.
 XX (BAYLOR) BAYLOR COLLEGE MEDICINE.
 XX (TEXAS) UNIV TEXAS SYSTEM.
 XX Benedict WF, Hu S, Xu H, Zhou Y;
 DR WPI: 1998-480788/41.
 DR P-PSDB: AAW69365.
 XX Retinoblastoma suppressor protein with N-terminal modification -
 PT inhibiting cellular proliferation, particularly cancer
 XX Claim 22; Page 142-147; 249pp; English.
 CC This sequence encodes a modified retinoblastoma tumour suppressor
 CC protein (Rb) of the human. The protein can be used to inhibit
 CC cellular proliferation, when coadministered with a p53 protein. The RbPS
 CC can be used for treating diseases characterised by abnormal cellular
 CC proliferation, particularly cancers. The RbPS have a broader spectrum of
 CC activity than wild type RbPS.
 XX Sequence 3455-35; 1154 A; 631 C; 527 G; 1044 T; 0 other;
 52

Alignment Scores:
 Pred. No.: 0 Length: 3455
 Score: 4499.00 Matches: 873
 Percent Similarity: 100.00% Conservative: 0

| | | |
|--|---------|---|
| Percent Similarity: | | 100.00% |
| Best Local Similarity: | 100.00% | |
| Query Match: | 99.89% | |
| DB: | 21 | |
| US-09-026-459a-31 (1-874) x AAA-29331 (1-4839) | | |
| QY | 2 | AspPheThrAlaLeuCysGlnLysLeuLysLeuProAspPheHisValArgGluArgAlaTrp 21 |
| DB | 43 | GAATTTACTGCAATATGTCAGAAATTAAGATACCAATCATGTCACAGAGAGAGCTGG 362 |
| QY | 22 | LeuThrTrpGlnLysValSerSerValAspGlyValLeuGlyGlyTyrLeuGlnLysLys 41 |
| DB | 63 | TAACATGGGAGAGATTCATCTGCTGGATGCGACTATGCGACGTTATATTCACAAAGAA 422 |
| QY | 42 | LysSerLeuLeuTrpGlyLysPheLeuAlaAlaValAspLeuAspGluMetSerPhe 61 |
| DB | 423 | AAAGCAAGCTGCGGCAATCTGTAATTCATGCGACAGTTGACCTACATCAGATGTCGTC 482 |
| QY | 62 | ThrPheThrGlnLeuGlnLysAsnIleGlnIleSerValHisLysPhePheAsnLeuLeu 81 |
| DB | 483 | ATTTTACTGAGCTACAGAAATACAGAAATACAGATGCTGCTTAACTTAACTACTA 542 |
| QY | 82 | LysGlnIleAspThrSerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyr 101 |
| DB | 543 | AAAGAAATTCATACCACTACCAAACTGATAATGCTATGTCACAGACGTTGCAACAGTAT 602 |
| QY | 102 | AspValLeuPheAlaLeuPheSerLysLeuGluArgThrCysGlnLeuIleTyrLeuThr 121 |
| DB | 63 | CACTGATGCTGAGCACTGACAGAAATGCAAAAGCACATGTCGAACTTATATATGACAA 662 |
| QY | 122 | GlnProSerSerThrSerThrGlnIleLeuAsnSerAlaLeuValLeuLysValSerTrp 141 |
| DB | 663 | CAAGCAAGATTCGATATCTAGTAAATTAATTCGATTCGCTGCTTAAAGTTCTCTTG 722 |
| QY | 142 | IleThrPheLeuLeuAlaLysGlyGlyGluValLeuGlnMetGluAspAspLeuValIleSer 161 |
| DB | 723 | ATCACATTTTATACCTAAAGCGGAGATTTACAAATGCAAGATGATCTGGGATTTTCA 782 |
| QY | 162 | PheGlnLeuMetLeuLysValLysAspLysPheIleLysLeuSerProMetLeuLeu 181 |
| DB | 783 | TTTACGTTAAATGCTGAGTCTGACATATTTATTAACCTTCACCTCCCATCTCTCC 842 |
| QY | 182 | LysGlnProLysThrAlaValIleProIleAsnGlySerProArgThrProArgArg 201 |
| DB | 843 | AAATACATATATAAAGCTGTTATACCTTAAATGCTGCTGCTGCAACACCGAGGGGA 902 |
| QY | 202 | GlyGlnAsnArgSerAlaArgIleAlaLysGlnLeuGlnAsnAspThrArgIleIleTyr 221 |
| DB | 903 | GGTACAAACAGGAGTCCAGGATAGCAAAACAACTAGAAAATGATACAGAAATATTCGA 962 |
| QY | 222 | ValLeuCysLysGlnIleGlnCysAsnIleAspGluValLysAsnValTyrPheLysAsn 241 |
| DB | 963 | TTTCTGTTAAAGCAATCAAGTAAATATAGATGAGGTCAAAATGTTTATTTCAAAAT 1022 |
| QY | 242 | PheIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValGlu 261 |
| DB | 1023 | TTTATACCTTTATGAAATTCCTGAGATTTGTACATCTTAATGGACTTCCAGAGTTGAA 1082 |
| QY | 262 | AsnLeuSerLysArgIleGlnIleLysLeuLysAsnLysAspLeuAspAlaArgLeu 281 |
| DB | 1083 | AAATCTCTAAATACAGAGAAATTTATCTTAAATTAAGATCTAGATGCAAAATTA 1142 |
| QY | 282 | PheLeuAspHisAspLysThrLeuGlnThrAspSerIleAspSerPheGluThrGlnArg 301 |
| DB | 1143 | TTTTCATCATCAATAAACTCTCAGATGATCTATAGACAGTTTTCGAAACACACAGA 1202 |
| QY | 302 | ThrProArgLysSerAsnLeuAspGluValAsnValIleProProHisIleProVal 321 |
| DB | 1203 | AAAGCAAGAAATGATCTGATGAGAGGAGTGAATGTAATCTCTCCACACACTCGATT 1262 |
| QY | 322 | AlaThrValMetAsnThrIleGlnIleLeuMetIleLeuAsnSerAlaSerAspGln 341 |
| DB | | TT |

| | | |
|----|------|--|
| DB | 1263 | AGCACGCTTATGAACACACTATCCAACAATTAATCATCATTTTAAATTCACCAAGTCAATCAA 1322 |
| QY | 342 | ProSerGluAsnLeuIleSerTyrPheAsnAsnCysThrValAsnProLysGluSerIle 361 |
| DB | 1323 | CCTTCAGAAATCTGATTTCCATTTTAACTACTGACAGTGAATCCAAAAGAAAGTATA 1482 |
| QY | 362 | IleLysArgValLysAspIleGlyIlePheLysCysLysPheAlaLysAlaValIle 381 |
| DB | 1383 | CTGAAGAGTGAAGGATATAGGATAGATGTTTAAAGAGAAATTTGCTAAAGCTGTGGGA 1442 |
| QY | 382 | GlnGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArg 401 |
| DB | 1443 | CAGGCTGTGTGCAAAATGCAATCACACACCAATACAAACTTGGACTTGGCTGCTGATACCGA 1502 |
| QY | 402 | ValMetGluSerMetLeuLysSerGlnGluArgLeuSerIleLeuAsnPheSerLys 421 |
| DB | 1503 | GTAATGCAATCCATGCTTAAATCAGAAAGAAAGCAATATGCAATTCAAATTTTAAAT 1562 |
| QY | 422 | LeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValIleMet 441 |
| DB | 1563 | CTTCTGAATGACCAATTTTCAATATGCTTTTATGGGCTGCTGCTTGGAGTGTAAATG 1622 |
| QY | 442 | AlaThrTyrSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPhePro 461 |
| DB | 1623 | CCACATACCAAGCAAGTACATGTCAGAACTTCATCTGCAACACATTTGCTGCTGCTG 1682 |
| QY | 462 | TrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrIleValIleGluSerPhe 481 |
| DB | 1683 | TGATTCGTAATGCTTAAATTTAAAGGCTTTGATTTTACAAAGTGAATGAAATTTT 1742 |
| QY | 482 | IleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisLeuGlnArgCysGluHis 501 |
| DB | 1743 | ATCAAGAGAGAGAGCACTTGACAGCAAGATGATAAATTTAGACGATGTGAATCAT 1802 |
| QY | 502 | ArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGln 521 |
| DB | 1803 | CGAATCACTCAACCTTGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 582 |
| QY | 522 | SerLysAspArgGlnGlyProThrAspHisLeuGlnSerAlaCysProLeuAsnLeuPro 541 |
| DB | 1863 | TCAAG 1922 |
| QY | 542 | LeuGlnAsnAsnHisThrAlaAspMetTyrLeuSerProValArgSerProLysLys 561 |
| DB | 1923 | CTCAGAAATTAATCAGACTGCGAGAGATATGATCTTCTCTGTAAGATCTGCAAGAA 1982 |
| QY | 562 | LysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAla 581 |
| DB | 1983 | AAAGGTCAACTACCGCTGTAATTTCTACTGCAAAATGCAAGACACACAGCAAGCAAG 2042 |
| QY | 582 | PheGlnThrGlnLysProLeuLysSerThrSerLeuSerLeuPheTyrIleValTyr 601 |
| DB | 2043 | TTCCAGACAG 2102 |
| QY | 602 | ArgLeuAlaTyrIleuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisProGln 621 |
| DB | 2103 | CGATGAGCTATCTGGGCTAAATATCTTCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2162 |
| QY | 622 | LeuGlnHisIleIleTrpThrLeuPheGlnHisThrLeuGlnAsnGlyTyrGlnLeuMet 641 |
| DB | 2163 | TTAACAATATCATCTGAG 2222 |
| QY | 642 | ArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleCysLysValLys 661 |
| DB | 2223 | AG 2282 |
| QY | 662 | AsnIleAspGlnLysPheLysIleIleValThrAlaIleLysAspLeuProHisAlaVal 681 |
| DB | 2283 | AAATATAGAGCTTAAATTCAAATCATTTGAAACAGATACAAAGAGATCTCTCTATGCTGT 2342 |
| QY | 682 | GlnGluThrPheLysArgValLeuIleLysLysLysGluTyrAspSerIleIleValPhe 701 |
| DB | 2343 | CAGAGAGATCAAGAGCTGTTTATGATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2402 |

222 ValLeuGlyLysGluHisGluCysAsnIleAspGluValLysAsnValTyrPheLysAsn 241
463 GTCCTCTGTAAGCAACATCAAGTAAATATAGATGACGTAAGAAATCTTATTTCAAAA 1022
242 PheIleProPheMetAsnSerLeuGlyLeuValThrSerAsnGlyLeuProGluValGlu 261
123 TTTATATCTTTTATGAAATCTCTTGACTTGTAAATCTAATGACATTCAGAGGTTCAA 1082
262 AsnLeuGlyLysAspGlyGluIleTyrLeuLysAsnLysAspLeuAspAlaArgLeu 281
183 AATCTCTTAAACCAACCAACAAATATCTTAAATAAAGATCTAGACCAATTA 1142
282 PheLeuAspHisAspLysThrLeuGluThrAspSerIleAspSerPheGluThrGlnArg 301
143 TTTTGGATCATGAATAAATCTCTACACATCTTATACACAGTTTGAACACACAGACA 1202
402 ThrProAlaLysSerAsnLeuAspGluGluValAsnValIleProProHisThrProVal 321
123 ACATACGAAAAAGTAACTTGAAGAGAGGTGAATGTAAATCTCTCCACACTCCAGTT 1262
422 ArgGluValMetAsnIleGluGlnLeuMetMetIleLeuAsnSerAlaSerAspGln 341
1263 AGCACTCTTATGAACATCAACCAAAATTAATGATGATTTAAATTCAGCAAGTGAAT 1322
442 ProSerGluAsnLeuLeuSerTyrPheAsnAsnCysThrValAsnProLysGluSerIle 361
123 GTCACAAAAATCTGATTCCTATTTTAAACATTCACACAGATTTAAATTCAGCAAGTGAAT 1382
462 LeuLysArgValLysAspIleGlyIlePheLeuGlyLysPheAlaLysAlaValGly 381
183 CTGAAACATGTAAGATATAGATATCATTTTAAAGAGAAATTTGTAAATCTGTGGA 1442
382 GlnGlyCysValGluIleGlySerGlnArgTyrLysLeuGlyValArgLeuTyrTyrArg 401
143 CAGGCTGTCTCAAAATGCAATACACAGGATACAAATCTGGACTTCGCTGTATTAACGA 1502
422 ValMetGluSerMetLeuLysSerGluGluArgLeuSerIleGlnAspPheSerLys 421
183 GTAAAGCAATCAATGCTTAAATACAAAGAACCAAGATTAATCAATCAAAATTTTACGAA 1562
422 LeuLeuAsnAspAsnIlePheHisMetSerLeuLeuAlaCysAlaLeuGluValIleMet 441
183 CTCTGATGATCAATTTTATATATGCTTTATTTGCGTGGCGCTTTAGGTTGTAATC 1622
442 AlaThrLysSerArgSerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPhePro 461
183 GTCATATATACCAAGATCATCTCAATCTTGTATCTTCAACACATTTGCTTTCCCA 1682
462 TrpIleLeuAsnValLeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPhe 481
183 TCGATCTGAAATGCTTAAATTTAAAGGCTTTGATTTTACAAAGTCATCGAAGTTT 1742
482 IleLysAlaGluGlyAsnLeuThrArgGluMetIleLysHisIleGluArgCysGluHis 501
173 ATCAAAAGAGAGGCAATCTGAAGCAAAATGATAAAACATTTAGAACGATGTGAACAT 1802
502 ArgIleMetGluSerLeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGln 521
183 TAAATCATGGAATGCTTCAATGCTCTCAATCTTATTTATTTATTTATTTAAACAA 1862
522 SerLysAspArgGlyGlyProThrAspHisLeuGluSerAlaCysProLeuAsnLeuPro 541
183 TAAAGGACCAACCAAGCATCAATGATCACTTGAATCTGCTTGTGCTGCTTAACTTCT 1922
542 LeuIleAsnAsnHisThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLys 561
123 TTTCAAAATTAATCACTCTACAGATATGATCTTCTCTGTAAGATCTCCAAAGAAA 1982
562 LysGlySerThrThrArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAla 581
183 AAAGCTTCAACTACCGCTGTAATTTCTACAGCAATGCAACACACACAAAGCAACTCAGCC 2042
582 PheGlnThrInLysProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyr 601

2043 TTCAGACCCAGAGCCATGAAATCTACCTCTCTTACAGCTTTTATAAAAAAGTAT 2102
602 ArgLeuAlaTyrLeuArgLeuAsnThrLeuCysGluArgLeuLeuSerGluHisArg 241
2103 CTGAGGCTATCTGAGCTAAATACATTTTGTGAAGGCTCTCTCTTACAGCCCAAA 2162
622 LeuGluHisIleIleIleTrpThrLeuPheGluHisThrLeuGlnAsnGluTyrGluLeuMet 2162
2163 TTACAACATATCATCTGCACCCCTTCCACACACACCCGACGAATGAGTATGAACTCA 2222
642 ArgAspArgHisLeuAspGlnIleMetMetCysSerMetTyrGlyIleTyrLysValLys 2222
2223 AGAAACAGCATTTTGACCAAAATATGATGCTTTCATGATGATGATGATGATGATGAT 2282
662 AsnIleAspLeuLysPheLysIleIleValThrAlaLysLysAspLeuProHisAlaVal 2282
2283 AATATACACTTAAATTTAAATTCATTTACAGATACAGATACAGATCTCTCTCTCTCT 2342
682 GlnGluThrPheLysArgValLeuLeuLysGluGluGluTyrAspSerIleIleValPhe 2342
2343 CAGGACATCAATCAACCTCTTTTGAACAAAGACAGGAGTATGATCTATATAGTAT 2402
702 TyrAsnSerValPheMetGlnArgLeuLysThrAsnIleLeuGlnTyrAlaSerIleArg 2402
2403 TATAACAGGCTCTTCAATGACAGACATGAAACAAATATTTTGCATGCTCTCTCTCT 2462
722 ProProThrLeuSerProIleProHisIleProArgSerProLysThrProSerSer 2462
2463 CCGCTACCTTGTACCAATACCTCATCTCTGAGGCTTACAGCTTCTCTCTCTCTCT 2522
742 ProLeuArgIleProGlyGlyAsnIleTyrIleSerProLeuLysSerProTyrLysIle 2522
2523 CCGCTACCTTGTACCAATACCTCATCTCTGAGGCTTACAGCTTCTCTCTCTCTCT 2582
762 SerGluGlyLeuProThrProThrLysMetThrProArgSerArgIleLeuValSerIle 2582
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Search completed: January 18, 2003, 08:37:31
Job time : 349.726 secs

15 JULY 2005

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10 919 GCACGATAGAAACCTGACAAATGATACAAAGATTTATTGAAATTTCTCTGTAAAGAA 978
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10 979 CATGAATGATATAGATGATGTCGAAATGTTTATTTCAAAAATTTTATACCTTTTATG 1038
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10 1099 TAAGAAAGAAATTTATCTTAAATAAAGATCTAGATGTCAGATTTATTTTGGATCATGAT 1158
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10 1219 AACTTCATTAAGAAAGCAAGTAAATTCCTCCACACACATCCAGCTTAAGGATGATTAAG 1278
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 RESULT 9
 AAV58440
 ID AAV58440 standard: DNA: 4555 bp.
 XX
 AC AAV58440;
 DT 02 DEC 1998 (first entry)
 DE Modified retinoblastoma tumour suppressor gene.
 XX
 KW Modified retinoblastoma tumour suppressor; RbP protein; cancer therapy;
 XX cellular proliferation inhibitor; ss.
 OS Homo sapiens.
 XX Key Location/Qualifiers
 FT CDS 7..2794


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1098 AAATCTCTGTGAATCTGTAAATATTAATGAGATTCAGAGGTTGAAATATCTTTCTAAACGA 1097
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RESULT 13
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XX
AC ABL62873;
XX
DT 15-MAY-2002 (first entry)
XX
DB Breast cancer related gene sequence SIO ID NO:1210.
XX
KW Human, cancer, colon, breast, ovary, oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilm's tumour; adenocarcinoma;
KW gene; ds.
XX
OS Homo sapiens.
XX
FN W200194629-A2.
XX

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 1398 GATATAGATATCTTTTAAAGAAATTTTAAAGATGATGATGATGATGATGATGATGATGATGAT 1457
 382 IleTyrSerGluThrTyrLeuGlyValArgLeuTyrTyrArgValMetGluSerMet 401
 1458 ATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1517
 402 LeuLysSerGluGluGluLeuLeuSerIleGluAsnPheSerLysLeuLeuAsnAspAsn 421
 1518 CTAAATCAGAAAG 1577
 422 IlePheHisMetSerLeuLeuAlaCysAlaLeuGluValIleMetAlaThrTyrSerArg 441
 1578 ATTTTCATATGCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1637
 442 SerThrSerGluAsnLeuAspSerGlyThrAspLeuSerPheProThrIleLeuAsnVal 461
 1638 AGTATATCAGAAATCTTCAATCTTCAATCTTCAATCTTCAATCTTCAATCTTCAATCTTCAATCT 1697
 462 LeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGly 481
 1698 CTAAATTTAAAAATCTTCAATCTTCAATCTTCAATCTTCAATCTTCAATCTTCAATCTTCAATCT 1757
 482 AsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMetGluSer 501
 1758 AACCTGACAAATCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1817
 502 LeuAlaIlePheSerAspGluThrPheAspLeuIleGlySerHisArgGlu 521
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 542 ThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysLysGlySerThrThr 561
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 562 ArgValAsnSerThrAlaAsnValGluThrGluAlaThrSerAlaPheGluThrGluLys 581
 1998 GAT 2057
 602 ProLeuLysSerThrSerLeuSerLeuPheTyrLysValIleArgLeuAlaTyrLeu 601

2058 CCATGAAATCTACCTCTCTTTCACCTTTTATAAAAAAGTGTACGGCTACCTATCTC 2117
 602 ArgLeuAsnThrLeuGlySerGluArgGluLeuSerGluHisThrGluLeuLeuHisIleIle 621
 2118 CGGTAAATATATTTGTGAAGCT 2177
 622 TrpThrLeuPheGluHisThrLeuGluAsnGluTyrGluLeuMetArgAspArgLeuLeu 641
 2178 TGCACCTTTTCCAGCATACACCTCTCCAGAAAGAGATGCAACTCAAGAGATACAGCAATTC 2237
 642 AspGluIleMetMetCysSerMetTyrGlyIleCysLysValLysAsnIleAspLeuLys 661
 2238 GATGAAATATATATTTGTGAAGCT 2297
 662 PheLysIleIleValIleThrAlaLysAspLeuProHisAlaValGluGluThrThrLys 681
 2298 TTCAAAATATTATTAAT 2357
 682 ArgValLeuIleLysGluGluThrAspSerIleValPheTyrAsnSerValPhe 701
 2358 CGTCTTTTGTATCAAAACAGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2417
 702 MetGluArgLeuLysThrAsnIleLeuGluThrAlaSerThrArgProProThrLeuSer 721
 2418 ATGAT 2477
 722 ProIleProHisIleLeuArgSerPyrTyrLysPheProSerSerProLeuArgIleArg 741
 2478 CCATATCTCTCATCT 2537
 742 GlyLysAsnIleTyrIleSerProLysSerProTyrLysIleSerGluGlyLeuPro 761
 2538 GGAGGGAATCT 2597
 762 ThrProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheLeu 781
 2598 ACACCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2657
 782 ThrSerGluGlyPheGluLysIleAsnGluMetValCysAsnSerAspArgValLeuLys 801
 2658 ACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2717
 802 ArgSerAlaGlySerAsnProLysProLysLysLysLysLysLysLysLysLysLysLysLys 821
 2718 AGAAGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2777
 822 GlySerAspGluAlaAspGlySerLysHisLeuProGlyGluSerLysPheGluGluLys 841
 2778 GAT 2837
 842 LeuAlaGluMetThrSerThrArgThrArgMetGluLysGluLysMetAsnAspSerMet 861
 2838 CTGAT 2897
 862 AspThrSerAsnLysGluLysLys 869
 2898 GATACCTCAACCAAGGAGAGAGAA 2921
 RESULT 14
 AAQ90059
 ID AAQ90059 standard; DNA; 2995 BP.
 XX AAQ90059;
 AC AAQ90059;
 DT 28-NOV-1995 (first entry)
 XX Retinoblastoma tumour suppressor gene.
 DE
 KW Recombinant: adenovirus; expression vector; fsc; small lung cancer;
 KW hepatocarcinoma; melanoma; retinoblastoma; sarcoma; sickle cell;
 KW anemia; Tay-Sach's disease; ss.
 XX

1679 AATTTTCAATGCTTTATTTGGGCGGCGCTTTGAGCTTGTAATGGCCACATATAGCAGA 1638
 442 SerThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProThrPheLeuAsnVal 461
 1699 ACTATATTCATCAAAATTTTGAATTTGAAAGATTTTGCCTTTTCAATGATTTGAAATG 1698
 462 LeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGly 481
 1699 GTTAAATTAAGAGCTTTGATTTTATCAAAAGTGATGAAAGTTTATCAAAAGCAAGGC 1758
 492 AsnLeuThrAlaGluMetIleLysIleLeuAlaGluArgCysGluHisArgIleLeuGluSer 501
 1679 AACTTGCACACAGACAAATCAATAAATTTACAACGATGATGACATCAATGGAATCC 1818
 502 LeuAlaTrpLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgGlu 521
 1819 GTTGCATGGCTCTGAAATTCACCTTTATTTGATCTTATTAATCAATCAAGGACCGAATA 1878
 522 GlyProThrAspHisLeuGlnSerAlaCysProLeuAsnLeuProLeuGlnAsnAsnHis 541
 1879 GAACTCAAGTGAATCACTTGAATCTGATTTGCTCTTAAATCTTCTCTCCAGATAATATCAG 1938
 542 ThrAlaAlaAspMetLysLeuSerProValArgSerProLysLysLysGlySerThrThr 561
 1939 ACTGCACGACAAATCAATCTTCCCTGCTTGAACATCTCCAAACAAAGAGCTTCAACTAG 1998
 562 ArgValAsnSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGlnThrGlnLys 581
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 582 ProLeuLysSerThrSerLeuSerSerPheGlyLysLysValTyrAlaLeuAlaTrpLeu 601
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 602 ArgLeuAsnThrLeuLysGluArgLeuLeuSerGluHisProGluLeuGluHisIleIle 621
 2119 GAGTAAATCAATCTGCAACCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2178
 622 TrpThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetArgAspArgHisLeu 641
 2179 TGGACGCTTTTCCAGACACACCGCTGCAATGATGATGATGATGATGATGATGATGATG 2238
 642 AspGlnLeuMetMetCysSerMetTrpGlyIleCysLysValIleAsnIleCysCulYS 661
 2239 GATCAATTAATGATGCTTTCATCTATGATATATGATATATGATATATGATATATGATAT 2298
 662 PheLysIleLeuValThrAlaLysAspLeuProHisAlaValGlnGluThrPheLys 681
 2299 TTTAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2358
 682 ArgValLeuIleLysGlnGluThrAspSerIleIleValPheTyrAsnSerValPhe 701
 2359 GGTGTTTATGATCAAAAGAGATATGATATATGATATATGATATATGATATATGATATG 2418
 702 MetLeuArgGluLysThrAsnIleLeuIleValIleValIleValIleValIleValIle 721
 2419 ATGCAAGATCAAGAAATATTTTGTATGATGATGATGATGATGATGATGATGATGATG 2478
 722 ProLeuProHisIleProArgSerProTyrLysPheProSerSerProLeuArgIlePro 741
 2479 GAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2538
 742 GlyGlyAsnIleTyrIleSerProLysSerProTyrLysLeuSerGluGluLeuPro 761
 2539 GGAAGAAATATATATTTTATGATGATGATGATGATGATGATGATGATGATGATGATG 2598
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 QY 922 GlySerAspGluAlaAspCysLysLysHisLeuTrpCysLysPheGlnGlnLys 841
 DB 2779 GCAATCAATCAACGACATGGAATTAACATCTCCAGGACAGTCCAAATTTCCACCACAA 2838
 QY 842 LeuAlaGluMetThrSerThrArgThrArgMetGluLysGlnLysMetAsnAspSerMet 861
 DB 2839 CTGCACAAAATGACTTCTACTCCAAACCAATGCAAAATGCAAAATGCAATGATGCAATG 2898
 QY 862 AspThrSerAsnLysGluGlnLys 869
 DB 2899 GATACCTTCAACCAACCAAGAGAAA 2922
 RESULT 15
 AAQ86398
 ID AAQ86398 standard: cDNA; 2995 BP.
 AC AAQ86398;
 XX 16-OCT-1995 (first entry)
 DI Human Rb110 cDNA.
 DE Rb110 gene; retinoblastoma; cancer; tumor suppressor protein;
 KW cell cycle, p110RB; ss.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FT CDS 139..2925
 FT /*tag- a
 XX WO9507708-A.
 XX 23-MAR-1995.
 XX 13-SEP-1994; 94WO-US10357.
 XX 13-SEP-1993, 94US-0121108.
 XX (CANI-) CANJI INC.
 PA (REG-) UNIV CALIFORNIA.
 XX Goodrich DW, Johnson D, Lee EYP, Lee W, Shepard HM,
 PI Wang NP;
 XX WP1: 1995-131179/17.
 DR P-PSDB; AAR71680.
 XX Admin. of a functional retinoblastoma polypeptide or protein -
 used to prevent and inhibit prim. and sec. retinoblastoma-linked
 cancers
 PS Disclosure: Fig.2; 163pp; English.
 XX By chromosomal walking from the esterase B gene on chromosome 13,
 CC the retinoblastoma susceptibility gene (RB) was identified on the
 CC basis of chromosomal location, homologous deletion and tumor-specific
 CC alterations in expression. Screening of cDNA libraries yielded clone
 CC RB-5 incorporating the complete RB cDNA sequence given in AAQ86398 and
 CC encoding a 116 140 kDa nuclear phosphoprotein named p110RB (AAQ86398).
 CC Use of recombinant p110RB will reduce the need for conventional
 CC radiotherapy of chemotherapy.
 XX
 SQ Sequence 2995 BP; 97% A; 61% C; 54% G; 41% T; 0 other;
 Alignment Scores:
 Pred. No.: 0 Length: 2995
 Score: 4446.50 Matches: 866


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CY 603 AsnLeuAspGluGluValAsnValIleProProHisThrProValArgThrValMetAsn 324
DB 1219 AAVTTGATGAGAGAGGAGGAGTAAATTCCTCCACACACTCCAGTTAGAGCTGTTATGAC 1278
QY 324 ThrIleGluLeuMetMetIleLeuAsnSerAlaSerAspGluProSerGluAsnLeu 343
DB 1279 AATATGCAACAAATAAAGAGATTTAAATTCAGCAAGTCAACCTTCAGAAAATCTG 1348
QY 344 IleSerTyrPheAsnAspGlyThrValAspProLysGluSerIleLeuLysAsnValLys 363
DB 1349 ATTTCGATTTTAAACATGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 1398
QY 363 AspIleLeuTyrIleGluSerLeuPheAlaValGluGluGluGluGluGluGluGlu 383
DB 1399 GATATGATATATTTTAAAGAGAAATTTGCTAAAGCTGTGGACAGAGTTGTCTGAA 1458
QY 384 IleGlySerGluAspTyrGluLeuGluValAlaLeuTyrTyrAlaValMetGluSerMet 403
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QY 403 LeuLysSerIleGluLeuArgLeuSerIleGluAsnPheSerLysLeuLeuAsnAspAsn 423
DB 1519 GTTAAATGAGAGAGAGAGATTTGCAATGCAATGCAATGCAATGCAATGCAATGCAAT 1578
QY 424 IlePheHisMetSerLeuLeuAlaGlyAlaLeuGluValValMetAlaThrTyrSerArg 443
DB 1579 ATTTTCATATGCTTTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1638
QY 444 SerThrSerIleAsnLeuAspSerGlyThrAspLeuSerPheProTyrIleLeuAsnVal 463
DB 1639 AATACATGCAAGATGCAATGCAAGATGCAAGATGCAAGATGCAAGATGCAAGATGCAAG 1698
QY 463 LeuAsnLeuLysAlaPheAspPheTyrLysValIleGluSerPheIleLysAlaGluGly 483
DB 1699 TTAATTTTAAATGCTTTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1758
QY 484 AsnLeuThrArgGluMetIleLysHisLeuGluArgCysGluHisArgIleMetGluSer 503
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QY 503 LeuAlaTyrPheSerAspSerProLeuPheAspLeuIleLysGluSerTyrAspArgGlu 523
DB 1819 GTTTCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1878
QY 523 ProThrAspHisLeuGluSerAlaLysProLeuAsnLeuProLeuGluAsnAsnHis 543
DB 1879 GGAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1938
QY 543 ThrAlaAlaAspMetTyrLeuSerProValArgSerProLysLysGlySerThrThr 563
DB 1939 ATGCAAGATATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1998
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DB 2059 GATATGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2118
QY 603 ArgLeuAsnThrLeuGluSerAlaValLeuSerGluHisProGluLeuHisIleThr 623
DB 2119 GATTAATATATTTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2178
QY 623 ThrLeuPheGluIleThrLeuGluAsnGluTyrGluLeuMetArgAspArgHisLeu 643
DB 2179 TGGACCTTTTTCAGATGCAAGATGCAAGATGCAAGATGCAAGATGCAAGATGCAAGATG 2238
QY 643 AsnIleLeuMetLysSerMetTyrGlyIleGlyLysValLysAsnIleAspLeuLys 663
DB 2239 GATTAATATATTTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2298
QY 663 PheLysIleThrValThrAlaTyrLysAspLeuPheHisAlaValGluGluGluGluGlu 683

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DB 2299 TCACAAATCATGTCACACACACACACACACACACACACACACACACACACACACACAC 2458
QY 684 ArgValLeuLysGluGluGluTyrAspSerIleIleValPheTyrAsnSerValPhe 703
DB 2459 CGGTGTTTCATCAACACACACACACACACACACACACACACACACACACACACACAC 2418
QY 704 MetGluArgLeuLysIleThrAsnIleGluGluTyrAlaSerThrArgProThrLeuSer 723
DB 2419 ATGACAGAGATGAAAATAATATTTTGGAGTAGTAGTAGTAGTAGTAGTAGTAGTAGTAG 2478
QY 724 ProIleHisIleThrArgSerIleTyrLysPheProSerSerPheLeuArgIlePro 743
DB 2479 GCAATACCTTCACATTCCTGCAACCTTACAACTTCCAGTTCACCTTACCGATTCCT 2538
QY 744 GlyGluAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerGluGluArgPro 763
DB 2539 GAGGAGACATATATATTCACCTTGAAGAGTCCATATAATAATTCAGAAAGGCTGCA 2598
QY 764 ThrProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGly 783
DB 2599 ATACCAATGAAAATGCTGCAACATGCAACATGCTTAGTATGAAATGAAATGAAATG 2658
QY 784 ThrSerGluLysPheGluLysIleAsnGluMetValCysAsnSerAspArgValIleLys 803
DB 2659 ACTTCGACACAGTTCACAAAATAATCAGATGCTATGTAACAGGAGTCCGCTGCTGCA 2718
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DB 2719 ATAACTGTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2778
QY 824 GlySerAspGluAlaAspGlySerTyrHisIleGluPheGlyGluSerLysPheGluGluLys 843
DB 2779 GATCAGATGAGGCAATGCAACATGCAACATGCAACATGCAACATGCAACATGCAACAT 2838
QY 844 LeuAlaGluMetThrSerThrArgThrArgMetGluLysGluLysMetAsnAspSerMet 863
DB 2839 CAGGACAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2898
QY 864 AspThrSerAsnLysGluGluLys 871
DB 2899 CATACCTCAACACACACACACACACACACACACACACACACACACACACACAC 2922
RESULT 5
AAAX90350
ID AAAX90350 standard; cDNA; 2995 BP.
XX
AC AAAX90350;
XX
XX 27-SNP-1999 (first entry)
XX Human p10-RB retinoblastoma tumour suppressor encoding cDNA.
XX Human p10-RB; retinoblastoma, tumour suppressor; gene therapy;
XX adenoviral protein; X-ray crystallographic expression vector;
XX cell cycle; p53, mitosis; cell death; apoptosis; thymidine kinase;
XX cancer; ss.
XX Homo sapiens.
XX
XX Key localisation/Qualifiers
XX CDS 139..2925
XX /start=
XX /product= "p10-RB"
XX /note= "retinoblastoma tumour suppressor"
XX
XX US5922210-A.
XX
XX 03-AUG-1999.
XX
XX 28-OCT-1997; 9708-0959638.
XX
XX 26-OCT-1994; 9406-0328673.
XX

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269 GCGGCTTTTGAACAAAGACAGCAGTATGATCTATATAGTATCTATTAACCTGGCTCTTC 2418
 704 MetGluArgLeuLysThrAspIleIleGlnIleValArgSerThrThrLeuSer 723
 2419 ATATACAGATGGAATATAATTTTGGATATGTTTACCCAGGCGCCCTTACCTTGCTCA 2478
 724 ThrIleProHisIleIleArgSerProGlyPheProSerSerProLeuArgIleLeu 743
 2479 CCAATACCTCAGATCTCTTGAAGAGCTTAAGATTCTCTAGTTCACCTTACGGATTCT 2538
 744 GlyLeuAspIleGlyIleLeuProLeuLeuSerProGlyPheSerLeuSerGlyLeuPro 763
 2539 GCAAGGAAATATATATATACCTCTTCAACAGACCAATATAAATTCACAGGCTCTCCCA 2598
 764 ThrProThrLysMetThrProArgSerArgIleGlnValSerIleGlyLeuSerPheLys 783
 2599 ACAGAAATAAATAAGAGCTGCAATATCAATATAGTATCAATTCGTCATATTCGCG 2658
 784 IleSerGlnLysPheGlnLysIleAsnGlnMetValCysAspSerAspArgValLeuLys 803
 2659 ACTTCTCAAGATCTTCAAAATATAATACATGGTATATTAACAGATCAATGCTTGTCTAA 2718
 804 ArgSerAlaArgLysSerAsnProGlyPheProGlyIleValArgPheAspIleLeu 823
 2719 ACAGAGCTCAAGAGAGATCTTCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2778
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 844 LeuAlaGlnMetIleSerThrArgThrArgMetGlnLysGlnLysMetAsnAspSerMet 863
 2839 CTGGAGAGAAATGATCTTATATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2898
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 2899 GATACCTCAACAGAGCAACAGAAA 2922
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Gregory RJ, Willis KN, Maneval DC;
 WFL 000: 289633/30.
 P-PSDB: AAE00689.
 XX
 PT New recombinant adenovirus expression vector having a gene encoding for
 a foreign protein and a partial or total deletion of the adenoviral
 protein IX DNA, useful in gene therapy for treating or reducing
 hyperproliferative cells -
 XX
 ES Disclosure, Fig 3: 49pp; English.
 XX
 CC The present cDNA sequence encodes retinoblastoma (RB) tumour suppressor
 protein, designated as p10RB.
 CC The invention relates to a recombinant adenovirus expression vector
 characterised by the partial or total deletion of the adenoviral protein
 IX DNA beginning at nucleotides 357 or 360 and ending at 4029-4050, and
 CC having a gene encoding a foreign protein such as tumour suppressor
 protein, p10RB (retinoblastoma) and p53. Adenovirus vector is used
 CC for screening tumour suppressor genes useful in gene therapy. The vector
 CC is particularly useful for treating or reducing hyperproliferative cell
 CC disorders such as thyroid hyperplasia, Grave's disease, psoriasis,
 CC benign prostatic hypertrophy, Li Fraumeni syndrome, various specifically
 CC hepatocellular carcinoma, neoplasms, leukemias, lymphomas, etc. to
 CC inhibit tumour proliferation or to accelerate particular related
 CC pathology such as sickle cell anaemia and Tay-Sachs disease. The vector
 CC is also useful for the safe recombinant production of diagnostic and
 CC therapeutic polypeptides and proteins.
 XX
 SO Sequence 2995 BP; 975 A; 618 C; 593 G; 809 T; 0 other;
 Alignment Scores:
 Pred. No.: 0 Length: 2995
 Score: 4447.50 Matches: 871
 Percent Similarity: 94.86% Substitutions: 0
 Best Local Similarity: 93.86% Mismatches: 0
 Query Match: 98.92% Indels: 57
 DB: 22 Gaps: 2
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 DB 139 ATGCGCGGCAAAACCCGCAAAACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 198
 QY 21 ProAlaIleProPhePheSerProGlyGlnGlnAspPheGlnGlnGlnGlnGlnGln 40
 DB 199 CCGGCG 258
 QY 41 AspGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 60
 DB 259 GAGTGGT 318
 QY 61 CysGlnLysGlnLysIleProAspHisValArgGluArgAlaIlePheIleThrProGlyLys 80
 DB 319 TGTCAAGAAATTAACAAATACCAATACCAATACCAATACCAATACCAATACCAATACCA 374
 QY 81 ValSerSerValAspGlyValLeuGlyGlyThrIleGlnGlnGlnGlnGlnGlnGln 100
 DB 379 GTTTCATCTGTGAGAGAGATATGCGAGGATATATCAAAACCAAAACCAAAACCAAA 438
 QY 101 IleCysIleThrGlnAlaAlaValAspGlnAspGlnMetSerPheThrPheThrGlnLeu 120
 DB 439 ATCTGTATCTTTATGACAGCAGTTCAGATAGAGATGAGATGAGATGAGATGAGATG 498
 QY 121 GlnLysAsnIleGlnIleSerValHisLysPhePheAsnMetLeuLysSerIleAspThr 140
 DB 499 CAGAAAAACATACAAATACAGTGTCCATATAATTTTAACTTACATAAAACAAATTCAT 558
 QY 141 SerThrLysValAsnAspAspAlaMetSerArgLeuLeuLeuLeuLeuLeuLeuLeu 160
 DB 559 AGTACCAAAAGTTTCATTAATGCTATGTCAGACAGTCTGCAAGAGATGATGATATCTT 618

1b 438 AATTGTAAGTATTATGGACAGTGGAGTACAGATGATGCTTCTACCTTTTACTGAGCTA 497
 2b 121 GlnLysAsnIleGlnIleSerValHisLysPhePheAsnLeuLeuLysGlnIleAspThr 140
 1b 439 CAAAAACATAGAAATACAGTGGCCATAAATCTTTAACTTACTTAAGAAATATGATACC 557
 2b 122 SerThrLysValAspAsnAlaMetSerArgLeuLeuLysLysTyrAspValLeuPheAla 160
 1b 440 AGTACCAAGTGTATATGATGTATGTAACATGCTTCAACAAAGTATATATATGTTGTGA 617
 2b 123 LeuPheSerLysLysLeuArgThrGlySerLeuLeuIleTyrLeuThrGlnProSerSerSer 180
 1b 441 CTTTCATCAAAATGGAAAGACAGTGGAACTTATATATTTACACAAACCCAGCAGTCG 677
 2b 124 IleSerThrGlnIleAsnSerAlaLeuValLeuLysValSerTrpIleThrPheLeuLeu 200
 1b 442 AATCTACATGAATATGAATGTGATGTATGCTTAAAGTTCCTGATCATCAATTTTATTA 737
 2b 125 AlaLysGlyGlnValLeuGlnMetGlnAspAspLeuValIleSerPheGlnLeuMetLeu 220
 1b 443 GCTAAAAGCAAAATATTAACATGAAATGATGATGATGATGATGATGATGATGATGAT 797
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 1b 444 GGGGCGCTGACATATTTATTAACATGCTACCTTCCCACTGCTCAAGAACCATATAAA 857
 2b 127 Thr-----GlySer----- 243
 1b 445 AAGTGTATTATATGATTAATGATGATGATGATGATGATGATGATGATGATGATGAT 917
 2b 128 GAGAGATAGCAAAATAGTAAATATGATGATGATGATGATGATGATGATGATGATGAT 977
 2b 129 ----- 243
 1b 446 CAGAAAGTAAATACAGAGTCAAAATATGTTATTTTCAAAATTTTATACCTTTTATG 1037
 2b 130 AsnSerLeuLysValIleSerAspGlyLeuProGlnValIleAsnLeuSerLysArg 263
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 2b 131 LysGlnGlnIleLysLysAsnLysAspLeuAspAlaArgLeuPheLeuAspHisAsp 283
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2b 421 TCT 443
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 2b 436 ProIlePheHisIlePheArgSerProLysPheProSerSerProLeuArgIlePro 743
 1b 471 GCAATACGATATGCTGTAATGCTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 2537
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 27 804 ArgSerAlaGluGlySerAsnProGlyLysProLeuLysLysLeuArgPheAspGln 823
 2718 ACAAATGCTCAAGTAAGTAAGTCTGCTAAAGGACATGAAAAAATACGTTTCATATGAA 2777
 27 824 GlySerAspGlnAlaAspGlySerGlySerLeuProGlnGlnSerLysPheGlnLys 843
 2778 GATATCATATTAAGTAGATGAATTAATATATGCTGCTAGAGAGTTCGCAAAATTCAGCAGAA 2837
 27 844 LeuAlaGlnMetThrSerThrArgPheArgMetGlnLysGlnLysMetAsnAspSerMet 863
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 27 864 AspThrSerAsnLysGlnLys 871
 2839 GATATCTTCAAAATCAAGCAGAA 2921
 27 871 09 MAY 2000 (first entry)
 27 871 Human androgen receptor coactivator 88 encoding cDNA SEQ ID NO: 7
 27 871 Human androgen receptor coactivator: ARA54; ARA55; ARA24; detection;
 27 871 androgenic; antiandrogenic; identification; prostate cancer; SS.
 27 871 Homo sapiens.
 27 871 Key location/qualifiers
 27 871 CDS 138..2924
 27 871 /start 4
 27 871 /product "Rb"
 27 871 /note: "androgen receptor coactivator"
 27 871 W020000415.2 A2.
 27 871 27 JAN 2000.
 27 871 16 JUL 1999; 9801 0515122.
 27 871 17 JUL 1998; 9805 0094249.
 27 871 14 SEP 1998; 9805 0100243.
 27 871 (GYPF) UNIV ROCHESTER.
 27 871 Chang C.
 27 871 WPI; 2000 101130/14.
 27 871 P US00; AAY28421.
 27 871 Need androgen receptor associated proteins used to detect androgenic
 27 871 or antiandrogenic activity in screening assays for candidate
 27 871 pharmaceutical molecules which promote or inhibit the activity
 27 871 claim 6; page 47 54; 56pp; English.

The present sequence encodes a human androgen receptor coactivator designated Rb. Androgen receptor coactivator proteins from the present invention can be used in screening assays to identify candidate pharmaceutical molecules for the ability to promote or inhibit the interaction of androgen receptors and androgen responsive elements to modulate androgenic activity. The identification and characterization of androgen receptor coactivators such as those of the invention will facilitate the development of screening assays to evaluate the potential efficacy of drugs in the treatment of prostate cancer.

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 Best Local Similarity: 93.86% Mismatches: 0
 Query Match: 98.92% Indels: 0
 DB: 21 Gaps: 2
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 QY 41 AspLeuProLeuValArgLeuGluPheGlnGlnThrGlnGlnProAspPheThrAlaLeu 60
 258 GAGCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 417
 QY 61 CysGlnLysLeuLysThrProAspPheValArgPheArgPheArgPheArgPheArg 80
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 41 ValSerSerValAlaProValLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100
 378 GTTTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 437
 QY 101 IleCysThrPheThrAlaAlaValAspLeuAspGlnMetSerPheThrPheThrGlnLeu 120
 438 ATCTGATCTTATGACAGCTGAGCTAGATGATGATGATGATGATGATGATGATGATG 497
 QY 121 GlnLysAsnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 140
 498 GAGAAAAACATAGAAATACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 557
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 558 AGTACCAAGTTCATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 617
 161 LeuPheSerLysLeuGlnArgThrCysGlnLeuLeuLeuLeuLeuLeuLeuLeuLeu 180
 618 CTCTTCAGCAAAATGGAAGAGCAATGTAATATATATATATATATATATATATATATAT 677
 QY 181 ThrSerThrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 200
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 QY 221 CysValLeuAspThrPheThrLeuLysLeuSerThrMetLeuLeuLeuLeuLeuLeu 240
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 QY 241 Thr -----GlySer
 858 ACATCTGTATATCATTAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 917
 QY 243 -----
 918 GTCAGGCAATCAAAACAAATAGAAAAATCAATAGAAATATATGAAATATATGAAAGAA 977
 QY 243 -----
 978 CATGAAATGATATATAGATGAGTGAAAAATGTTTATTTAAAAATTTTATATATTTTAT 1037
 QY 244 AsnSerLeuGlyLeuValThrSerAsnGlyLeuValThrGlnGlnGlnGlnGlnGln 264


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00 243 ..... 243
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26 246 AATCTCTGGACCTGGTAAACATCTAAAGACCTCCAGAGGTGAAAACTCTCTAAACGA 1097
32 264 TysThrGlnGlyLeuLeuLysAsnLeuAspLeuAspAlaArgLeuPheLeuAspHisAsp 283
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44 284 LysThrLeuGlnThrAspSerIleAspSerPheGlnArgGlnArgThrProArgLysSer 303
50 1158 AAAATCTTCAGACTGATTCTATATATAGTTTGAATATAGATCAATCAATCAATCAAT 1217
56 304 AsnLeuAsnGlnValAsnValIleProProHisThrProValArgThrValMetAsn 323
62 1218 AAGCTTGAAGAAAGAGTGAATGAAATTCCTCCACACACTCCAGTTAGGACTGTTATGAAC 1277
68 324 ThrIleGlnGlnLeuMetMetIleLeuAsnSerAlaSerAspGlnProSerGlnAsnLeu 343
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116 404 LysSerGlnGlnLeuArgLeuSerIleGlnAsnPheSerLysLeuLeuAsnAspAsn 423
122 1518 CTAAATCAAGAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1577
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134 1578 ATCTTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1637
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146 1637 AGTACATCTCAGAAATCTTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 1697
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218 1997 CGTGTAAATCTTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2057
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2238 CATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2297
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2898 GATACCTCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT 2921
2921
RESULT 14
AAQ90059
ID AAQ90059 standard; DNA; 2995 bp.
XX
AC AAQ90059;
XX
28-NOV-1995 (first entry)
DE Retinoblastoma tumour suppressor gene.
KW Recombinant: adenovirus; expression vector; T85; small lung cancer;
KW hepatocellular carcinoma; melanoma; retinoblastoma; sarcoma; sickle cell;
KW anaemia; Tay-Sachs disease; ss.
XX

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| | | | |
|---|---|--|------|
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| QY | 824 | GlySerAspGluAlaAspGlySerLysHisLeuPheGlyGluSerLysPheGluGluLys | 843 |
| DQ | 2779 | GGATCATATTAAGTAAATGAAATTAATATCTTGTAGTAGACGTTCAATTTCTAGTAAA | 2848 |
| QY | 844 | LeuAlaGluMetThrSerThrArgThrArgMetGlnLysGlnLysMetAspSerMet | 863 |
| DQ | 2839 | TGTGTCATAAATATATTTCTATCAAAATATCAAAATATCAAAATATCAAAATATCAAAAT | 2898 |
| QY | 864 | AspThrSerAsnLysGluGluLys | 871 |
| DQ | 2899 | CATACCTCAACCAACCAACAGAAA | 2922 |
| RESULT 15 | | | |
| ID | AAQ04713 | standard; cDNA; 2994 bp. | |
| XX | AAQ04713; | | |
| AC | AAQ04713; | | |
| DT | 11-OCT-1990 (first entry) | | |
| XX | | | |
| DE | Cancer suppressing gene (CSG). | | |
| XX | | | |
| KW | Cancer; cancer suppressing gene; CSG; 13q14; retinoblastoma; | | |
| KX | RB; DS. | | |
| OS | Homo sapiens. | | |
| E4 | KEY Location/Qualifiers | | |
| FT | CDS 139..2922 | | |
| FT | /tag= a | | |
| XX | | | |
| FN | W09005180-A. | | |
| XX | | | |
| FD | 17-MAY-1990. | | |
| XX | | | |
| PE | 30-OCT-1989; HAWO-000480R | | |
| XX | | | |
| FE | 31-OCT-1989; 88US 0265829. | | |
| XX | | | |
| PA | (RBC) UNIV OF CALIFORNIA. | | |
| XX | | | |
| FI | Lee WH, Huang HS. | | |
| XX | | | |
| B9 | WPI; 1990-178822/23. | | |
| DR | P-PSDB; AAR05305. | | |
| XX | | | |
| PT | Controlling cancer - | | |
| TI | by replacing ineffective cancer suppressing gene with cloned, | | |
| PT | active gene. | | |
| XX | | | |
| PS | Claim 35; Page 86; 105pp; English. | | |
| XX | | | |
| CC | Gene is taken from human chromosome 13q14 retinoblastoma (RB) cDNA. | | |
| CC | By installing a working CSG, safe and specific treatment and | | |
| CC | prophylaxis can be given to cancer patients. | | |
| XX | | | |
| SQ | Sequence 2994 BP: 974 A; 618 C; 593 G; 809 T; 0 other; | | |
| Alignment Scores: | | | |
| pred No.: | 0 | length: | 2994 |
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| Percent Similarity: | 93.75% | Conservative: | 0 |
| Best Local Similarity: | 94.75% | Mismatches: | 1 |
| Query Match: | 98.72% | Gaps: | 57 |
| DH: | 11 | | 2 |
| US-09-026-459A-49 (1-871) x AAQ04713 (1-2994) | | | |

| | | |
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| 2304 | ATATVALLLELYSGLUAGLUATPASPSEFILLEVALPHEYRASNSEVALPHE | 703 |
| 2309 | CGTGTTTGGATCAAAAGAAAGAAATATCTTATTATAGTATCTATATACGTGCTTC | 2418 |
| 2314 | MetGlnArgLeuLysThrAsnIleGlnIlyrAlaSerThrArgProProThrLeuSer | 723 |
| 2419 | ATGAGAAATCAAAATATATTTGATATCTTCTCAATCAAGAAATCAATTTCTCA | 2478 |
| 2424 | ProIleProHisIleProArgSerProTyrGlySerPheProSerProLeuArgIlePro | 743 |
| 2479 | CAAAACATCTACATCTCTCTCAAGGCTTACAAAGTCTCTAGTTCACCTTACCGATTCCT | 2538 |
| 2484 | GLYGLYASCTYRILESERPROLEULYSSERPROTYRLYSILESERGLULYLEUPRO | 763 |
| 2539 | GGAGAGAAATCTATATATTAAGGATCAAGATATATAAAATTTCAAAAGCTTCTCA | 2598 |
| 2544 | ThrProThrLysMetThrProArgSerArgIleLeuValSerIleGlyGluSerPheGly | 783 |
| 2599 | ATACCAACAAAAATGACTCAAGATATCAAGATCTTATATCAATTTGTTAAATATTGAA | 2658 |
| 2604 | ThrSerGluLysPheLeuLysIleAsnGlnMetValGlyAsnSerAspArgValLeuLys | 803 |
| 2659 | ACCTCTACACTTCTCAAAAAAIAAAACATGCTATGTAAACAGCAAGCTGTGCTCAAA | 2718 |
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| 2779 | GGATCAGATGAAGACAGATGGAAGATTAATATCTCTCAAGCAATTTCAAAATTTCA | 2838 |
| 2834 | LeuAlaIleMetThrSerThrArgMetGlnLysGlnLysMetAsnAspSerMet | 863 |
| 2839 | CTGGGCACAAAACACCTCTACCTCAAGCAACAGAAATCCAAAGCAGAAAAAGAAATCATACCATC | 2898 |
| 2844 | AspThrSerAsnLysGluGluLys | 871 |
| 2899 | TAATCTCAAAACAAAGAAAGAAA | 2922 |

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Index time : 405.762 secs

Genware version 6.1.4
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OR nucleic nucleic search, using SW model

Run on: January 16, 2003, 15:20:22 / Search time 69,4298 seconds
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14944,909 Million cell updates/sec

File: us-09-026-459a-48
Perfect score: 5084
Sequence: 1 CCGGTCATCGGGGAAAC.....AAATGAGATTTATTCATAGT 3493

Scoring table: IDENTITY_NP
Gapop 10.0 / Gapext 1.0

Searched: 441,662 seqs, 15,668,881 residues

Total number of hits satisfying chosen parameters: 862724

Minimum hit seq length: 0
Maximum hit seq length: 200000000

Post processing: Minimum Match 6%
Maximum Match 100%
Listing first 45 summaries

Database: Issued Patents NA: *
1: 6002673 (1999) 2: 600959A (2000) seq: *
3: 6011111 (1999) 4: 6011111 (1999) seq: *
5: 6011111 (1999) 6: 6011111 (1999) seq: *
7: 6011111 (1999) 8: 6011111 (1999) seq: *
9: 6011111 (1999) 10: 6011111 (1999) seq: *

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|-----------------------------------|
| 1 | 2864 | 84.7 | 4242 | 1 | US-08-038-760-1 Sequence 1, App11 |
| 2 | 2951 | 84.7 | 4242 | 1 | US-08-038-760-2 Sequence 2, App11 |
| 3 | 2864 | 84.7 | 4242 | 2 | US-08-038-760-1 Sequence 1, App11 |
| 4 | 2864 | 84.7 | 4242 | 2 | US-08-038-760-2 Sequence 2, App11 |
| 5 | 2951 | 84.7 | 4242 | 3 | US-08-038-760-1 Sequence 1, App11 |
| 6 | 2951 | 84.7 | 4242 | 3 | US-08-038-760-2 Sequence 2, App11 |
| 7 | 2951 | 84.7 | 4242 | 4 | US-08-038-760-1 Sequence 1, App11 |
| 8 | 2951 | 84.7 | 4242 | 4 | US-08-038-760-2 Sequence 2, App11 |
| 9 | 2951 | 84.7 | 4242 | 5 | US-08-038-760-1 Sequence 1, App11 |
| 10 | 2951 | 84.7 | 4242 | 5 | US-08-038-760-2 Sequence 2, App11 |
| 11 | 2951 | 84.7 | 4242 | 6 | US-08-038-760-1 Sequence 1, App11 |
| 12 | 2951 | 84.7 | 4242 | 6 | US-08-038-760-2 Sequence 2, App11 |
| 13 | 2951 | 84.7 | 4242 | 7 | US-08-038-760-1 Sequence 1, App11 |
| 14 | 2951 | 84.7 | 4242 | 7 | US-08-038-760-2 Sequence 2, App11 |
| 15 | 2951 | 84.7 | 4242 | 8 | US-08-038-760-1 Sequence 1, App11 |
| 16 | 2951 | 84.7 | 4242 | 8 | US-08-038-760-2 Sequence 2, App11 |
| 17 | 2951 | 84.7 | 4242 | 9 | US-08-038-760-1 Sequence 1, App11 |
| 18 | 2951 | 84.7 | 4242 | 9 | US-08-038-760-2 Sequence 2, App11 |
| 19 | 2951 | 84.7 | 4242 | 10 | US-08-038-760-1 Sequence 1, App11 |
| 20 | 2951 | 84.7 | 4242 | 10 | US-08-038-760-2 Sequence 2, App11 |
| 21 | 2951 | 84.7 | 4242 | 11 | US-08-038-760-1 Sequence 1, App11 |
| 22 | 2951 | 84.7 | 4242 | 11 | US-08-038-760-2 Sequence 2, App11 |
| 23 | 2951 | 84.7 | 4242 | 12 | US-08-038-760-1 Sequence 1, App11 |
| 24 | 2951 | 84.7 | 4242 | 12 | US-08-038-760-2 Sequence 2, App11 |
| 25 | 2951 | 84.7 | 4242 | 13 | US-08-038-760-1 Sequence 1, App11 |
| 26 | 2951 | 84.7 | 4242 | 13 | US-08-038-760-2 Sequence 2, App11 |
| 27 | 2951 | 84.7 | 4242 | 14 | US-08-038-760-1 Sequence 1, App11 |

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| 28 | 44 | 1.4 | 5652 | 1 | US-07-867-106-2 | Sequence 2, App11 |
| 29 | 42.8 | 1.4 | 615 | 4 | US-08-998-416-186 | Sequence 186, App11 |
| 30 | 42.6 | 1.4 | 2156 | 4 | US-09-254-8278-4 | Sequence 4, App11 |
| 31 | 42.4 | 1.4 | 1186 | 2 | US-08-731-722-9 | Sequence 9, App11 |
| 32 | 42.4 | 1.4 | 1776 | 1 | US-08-722-001-29 | Sequence 29, App11 |
| 33 | 42 | 1.2 | 665 | 2 | US-08-883-799A-6 | Sequence 6, App11 |
| 34 | 42 | 1.2 | 1864 | 4 | US-09-468-265-4 | Sequence 4, App11 |
| 35 | 41.8 | 1.2 | 1679 | 4 | US-09-406-060-1 | Sequence 1, App11 |
| 36 | 41.4 | 1.2 | 19124 | 2 | US-08-487-8278-14 | Sequence 14, App11 |
| 37 | 41.2 | 1.2 | 921 | 4 | US-08-998-416-541 | Sequence 541, App11 |
| 38 | 41.2 | 1.2 | 867 | 4 | US-08-998-416-288 | Sequence 288, App11 |
| 39 | 41.2 | 1.2 | 2860 | 2 | US-08-765-947-7 | Sequence 7, App11 |
| 40 | 40.8 | 1.2 | 1144 | 1 | US-08-014-944A-1 | Sequence 1, App11 |
| 41 | 40.8 | 1.2 | 1144 | 1 | US-08-486-421-2 | Sequence 2, App11 |
| 42 | 40.8 | 1.2 | 1144 | 1 | US-08-470-511-2 | Sequence 2, App11 |
| 43 | 40.8 | 1.2 | 1144 | 2 | US-08-486-809-2 | Sequence 2, App11 |
| 44 | 40.8 | 1.2 | 2140 | 1 | US-08-534-698-1 | Sequence 1, App11 |
| 45 | 40.8 | 1.2 | 2140 | 1 | US-08-228-952-1 | Sequence 1, App11 |

ATTACHMENTS

RESULT 1
US-08-038-760-1
Sequence 1, Application US/08048760
Patent No. 5496731
GENERAL INFORMATION:
APPLICANT: Xu, Hong Li
INVENTOR: Xu, Hong Li
ATTORNEY: Benedict, William F.
TITLE: INVERTER, Radio Spectrum Tuner Suppressor, Radio Products and
METHOD OF OPERATION: Methods of Radio Suppressor Gene Therapy.
NUMBER OF SEQUENCES: 4
CROSS-REFERENCE: Abstract:
ADDRESS: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ATTACHMENT NUMBER: US/08048760
FILING DATE: 19930425
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: POISSANT, Brian M
REGISTRATION NUMBER: 28,462
REFERENCE/AGENT NUMBER: 2429, 245, 999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4242 base pairs
TYPE: NUCLEIC ACID
STRANDNESS: double
DIRECTION: not relevant
MOLECULE TYPE: DNA
FEATURE:
NAME/KEY: CDS
LOCATION: 19..2469
US-08-038-760-1

Query Match: 84.7%, Score 2864, DB 1, Length 4242
Best Local Similarity: 94.5%, Prod. No. 0
Matches 3048, ClustalScore 6, Mismatch 6, Indel 171, Gaps 13

DB 1574 ACAACATTTTCATATGTCCTTTATTTGGCTGGCTCTTGAGGTGTAAATGGCCACATATA 1633
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DB 1634 GCAAGACAGTACGTCAGAACTGATGATGCGAAGCAGATTTGCTTTCCCAATGGATTGGA 1693
QY 1691 ATGGGTGATTAATTAAGAGTTTGATTTTAAATATATGTAAGAGTTTATTAAGAGAG 1750
DB 1694 ATGGGTGATTAATTAAGAGTTTGATTTTAAATATATGTAAGAGTTTATTAAGAGAG 1753
QY 1751 AAGGTAACTTGACAGAGAGAAATGATTAAGAGAGTTTATTAAGAGAGTTTATTAAGAGAG 1810
DB 1754 AAGGTAACTTGACAGAGAGAAATGATTAAGAGAGTTTATTAAGAGAGTTTATTAAGAGAG 1813
QY 1811 AATGCTTGACAGAGAGAAATGATTAAGAGAGTTTATTAAGAGAGTTTATTAAGAGAG 1870
DB 1814 AATGCTTGACAGAGAGAAATGATTAAGAGAGTTTATTAAGAGAGTTTATTAAGAGAG 1873
QY 1871 GAG 1930
DB 1874 GAG 1933
QY 1931 ATGACATGACAG 1990
DB 1934 ATGACATGACAG 1993
QY 1991 ATGACATGACAG 2050
DB 1994 ATGACATGACAG 2053
QY 2051 AG 2110
DB 2054 AG 2113
QY 2111 ATGACATGACAG 2170
DB 2114 ATGACATGACAG 2173
QY 2171 ATGACATGACAG 2230
DB 2174 ATGACATGACAG 2233
QY 2231 ATGACATGACAG 2290
DB 2234 ATGACATGACAG 2293
QY 2291 ATGACATGACAG 2350
DB 2294 ATGACATGACAG 2353
QY 2351 ATGACATGACAG 2410
DB 2354 ATGACATGACAG 2413

DB 2654 TCGAGAGTTTCAGAGAGTTTCAGAGAGTTTCAGAGAGTTTCAGAGAGTTTCAGAGAG 2713
QY 2411 TCAAAAGAGTTTCAGAGAGTTTCAGAGAGTTTCAGAGAGTTTCAGAGAGTTTCAGAGAG 2470
DB 2714 TCAAAAGAGTTTCAGAGAGTTTCAGAGAGTTTCAGAGAGTTTCAGAGAGTTTCAGAGAG 2773
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QY 2591 GATGAGTTTCAGAGAGTTTCAGAGAGTTTCAGAGAGTTTCAGAGAGTTTCAGAGAG 2650
DB 2894 GATGAGTTTCAGAGAGTTTCAGAGAGTTTCAGAGAGTTTCAGAGAGTTTCAGAGAG 2953
QY 2651 TCAAAAGAGTTTCAGAGAGTTTCAGAGAGTTTCAGAGAGTTTCAGAGAGTTTCAGAGAG 2713
DB 2954 TCAAAAGAGTTTCAGAGAGTTTCAGAGAGTTTCAGAGAGTTTCAGAGAGTTTCAGAGAG 2953

RESULT 6

US-08-801-092-3
Sequence 3, Application US/08801092
Patent No. 6074850
GENERAL INFORMATION:
APPLICANT: Antelman, Douglas
APPLICANT: Gregory, Richard J.
APPLICANT: Wills, Kenneth N.
TITLE OF INVENTION: Tissue Specific Expression of
TITLE OF INVENTION: Retinoblastoma Protein
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08801092
FILING DATE: 14-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/751,517
FILING DATE: 15-NOV-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: FILLIS, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/FILE NUMBER: 03-930 001020
TELEPHONE: 415-576-0200
TELEFAX: 703-576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2994 base pairs
TYPE: nucleic acid
STANDARDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-801-092-3

Query Match 74.0% Score 2502.67 DP 37 Length 2994
Best Local Similarity 93.9% Pred. No. 0
Matches 2666, Conservative 0, Mismatches 4, Indels 171, Gaps 1

Genome version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

CM nucleic nucleic search using sw model

Run on: January 16, 2003 16:00:22 : Search time 69.9977 seconds
(without alignments)
14944,909 Million cell updates/sec

Filter: US-09-026-459A-46

Perfect score: 4377

Sequence: 1 GGGGATGCGGGGAAAAA.....AAATGAGGATTAATGATAGT 4377

Scoring tables: IDENTITY NUC

Gapop 10.0, Capopt 1.0

Searches: 44162 seqs, 15336961 residues

Total number of hits satisfying chosen parameters: 98274

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : Issued Patents, NA:*
- 1: /comz_6/prodata/1/na/5A_00MB.seq.*
 - 2: /comz_6/prodata/1/na/5B_00MB.seq.*
 - 3: /comz_6/prodata/1/na/6A_00MB.seq.*
 - 4: /comz_6/prodata/1/na/6B_00MB.seq.*
 - 5: /comz_6/prodata/1/na/pepMS_00MB.seq.*
 - 6: /comz_6/prodata/1/na/backfile1.seq.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|---------------------|-------------------|
| 1 | 285.2 | 84.5 | 3242 | US-08-048-760-1 | Sequence 1, Appl |
| 2 | 285.2 | 84.5 | 3242 | US-08-048-760-2 | Sequence 2, Appl |
| 3 | 285.2 | 84.5 | 3242 | US-08-470-091-1 | Sequence 1, Appl |
| 4 | 285.2 | 84.5 | 3242 | US-08-470-091-2 | Sequence 2, Appl |
| 5 | 2490.6 | 74.8 | 2994 | US-08-254-429-2 | Sequence 2, Appl |
| 6 | 2490.6 | 74.8 | 2994 | US-08-801-092-3 | Sequence 3, Appl |
| 7 | 2490.6 | 74.8 | 2994 | US-09-415-113-3 | Sequence 3, Appl |
| 8 | 2487.6 | 74.7 | 2994 | US-08-482-627-4 | Sequence 4, Appl |
| 9 | 2487.6 | 74.7 | 2994 | US-08-959-638-7 | Sequence 7, Appl |
| 10 | 2487.4 | 74.7 | 2994 | US-08-104-057-1 | Sequence 1, Appl |
| 11 | 2486.6 | 74.6 | 2994 | US-08-428-673A-2 | Sequence 7, Appl |
| 12 | 68.8 | 2.0 | 2808 | US-07-708-962-1 | Sequence 1, Appl |
| 13 | 68.2 | 2.0 | 3249 | US-08-106-493A-1 | Sequence 1, Appl |
| 14 | 68.2 | 2.0 | 3249 | US-08-429-264-1 | Sequence 1, Appl |
| 15 | 68.2 | 2.0 | 4853 | US-08-852-883-1 | Sequence 1, Appl |
| 16 | 68.2 | 2.0 | 4853 | US-08-852-877-1 | Sequence 1, Appl |
| 17 | 65.6 | 1.9 | 2808 | US-08-152-7218-1 | Sequence 1, Appl |
| 18 | 59 | 1.7 | 7218 | US-08-242-663-14 | Sequence 14, Appl |
| 19 | 57 | 1.5 | 4747 | US-09-213-2930-2 | Sequence 2, Appl |
| 20 | 44.6 | 1.3 | 1803 | US-09-144-0010-799 | Sequence 799, App |
| 21 | 44.6 | 1.3 | 15363 | US-08-961-527-139 | Sequence 139, App |
| 22 | 44.4 | 1.3 | 19674 | US-09-431-638-651 | Sequence 651, App |
| 23 | 44 | 1.3 | 19124 | US-08-487-8268-13 | Sequence 13, Appl |
| 24 | 43.8 | 1.3 | 1056 | US-09-144-0010-1550 | Sequence 1550, Ap |
| 25 | 44.2 | 1.3 | 509 | US-06-432-607-202 | Sequence 202, App |
| 26 | 44.2 | 1.3 | 509 | US-09-465-786-202 | Sequence 202, App |
| 27 | 44.2 | 1.3 | 509 | US-09-449-418-202 | Sequence 202, App |

| | | | | | | |
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| 28 | 43.2 | 1.3 | 509 | 4 | US-09-432-616A-202 | Sequence 202, App |
| 29 | 43.2 | 1.3 | 509 | 4 | US-09-432-149A-202 | Sequence 202, App |
| 30 | 43 | 1.3 | 5852 | 1 | US-07-867-106-2 | Sequence 2, Appl |
| 31 | 42.8 | 1.3 | 615 | 4 | US-08-998-416-186 | Sequence 186, App |
| 32 | 42.6 | 1.3 | 1189 | 1 | US-08-407-591-2 | Sequence 2, Appl |
| 33 | 42.6 | 1.3 | 2606 | 4 | US-09-244-827B-3 | Sequence 1, Appl |
| 34 | 42.4 | 1.3 | 1186 | 2 | US-08-741-722-5 | Sequence 5, Appl |
| 35 | 42.4 | 1.3 | 1776 | 2 | US-08-722-701-23 | Sequence 29, Appl |
| 36 | 42 | 1.2 | 645 | 2 | US-08-893-795A-46 | Sequence 46, Appl |
| 37 | 42 | 1.2 | 1864 | 4 | US-09-468-265-4 | Sequence 4, Appl |
| 38 | 41.8 | 1.2 | 1679 | 4 | US-09-406-060-1 | Sequence 1, Appl |
| 39 | 41.4 | 1.2 | 19124 | 2 | US-08-487-8268-13 | Sequence 13, Appl |
| 40 | 41.2 | 1.2 | 821 | 4 | US-08-998-416-186 | Sequence 186, App |
| 41 | 41.2 | 1.2 | 837 | 4 | US-08-998-416-186 | Sequence 186, App |
| 42 | 41.2 | 1.2 | 2236 | 2 | US-08-254-429-2 | Sequence 2, Appl |
| 43 | 40.8 | 1.2 | 1144 | 1 | US-08-014-944A-1 | Sequence 1, Appl |
| 44 | 40.8 | 1.2 | 1144 | 1 | US-08-486-421-2 | Sequence 2, Appl |
| 45 | 40.8 | 1.2 | 1144 | 1 | US-08-470-911-2 | Sequence 2, Appl |

ALIGNMENTS

RESULT 1
US-08-048-760-1
: Sequence 1, Application US/08048760
: Patent No. 5496731
: GENERAL INFORMATION:
: APPLICANT: XU, Hong-Ji
: APPLICANT: Bi, Shi-Xue
: APPLICANT: Benedic, William F.
: TITLE OF INVENTION: Broad Spectrum Tumor Suppressor Genes, Gene Products and
: TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.
: NUMBER OF SEQUENCES: 4
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Pennie & Edmonds
: STREET: 1155 Avenue of the Americas
: CITY: New York
: STATE: New York
: COUNTRY: U.S.A.
: ZIP: 10036, 2711
: COMPUTER TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC DOS/MS-DOS
: SOFTWARE: Patent to Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/048,760
: FILING DATE: 19903325
: CLASSIFICATION: 424
: ATTORNEY/AGENT INFORMATION:
: NAME: Poussant, Brian M
: REGISTRATION NUMBER: 28,462
: REFERENCE/RET NUMBER: 7409, 02, 999
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 790 9090
: TELEFAX: (212) 809,974,78864
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 3242 base pairs
: TYPE: NUCLEIC ACID
: STRANDEDNESS: double
: TOPOLOGY: not relevant
: MOLECULE TYPE: DNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 19..2465
US-08-048-760-1

Query Match: 84.5%, Score: 285.2, DB ID: 10041, 4242
Best Local Similarity: 94.4%, Prod. No.: 1
Matches: 4042, Conservation: 5, Labels: 177, Gaps: 1

1354 ACAAATTTCATATGCTTTATATGGGAGGCTTTTGGAGTTTAAATGACCAATATA 1633
1355 GCAAGATGACATGACAAATGCTGATGCTGGAACACATTTGCTTTCCCATGATTCGA 1384
1356 CCAAAATGATGCTGAAATGCTGATGCTGGAACACATTTGCTTTCCCATGATTCGA 1693
1357 AATGCTGCTTAAATTTAAAGGCTTTGATTTTACAAAGTGTGAAAGTGTTCATCAAGGAG 1444
1358 AATGCTGCTTAAATTTAAAGGCTTTGATTTTACAAAGTGTGAAAGTGTTCATCAAGGAG 1753
1359 AATGCTGCTTAAATTTAAAGGCTTTGATTTTACAAAGTGTGAAAGTGTTCATCAAGGAG 1504
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1365 AATGCTGCTTAAATTTAAAGGCTTTGATTTTACAAAGTGTGAAAGTGTTCATCAAGGAG 1684
1366 AATGCTGCTTAAATTTAAAGGCTTTGATTTTACAAAGTGTGAAAGTGTTCATCAAGGAG 1993
1367 AATGCTGCTTAAATTTAAAGGCTTTGATTTTACAAAGTGTGAAAGTGTTCATCAAGGAG 1744
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1369 AATGCTGCTTAAATTTAAAGGCTTTGATTTTACAAAGTGTGAAAGTGTTCATCAAGGAG 1804
1370 AATGCTGCTTAAATTTAAAGGCTTTGATTTTACAAAGTGTGAAAGTGTTCATCAAGGAG 2113
1371 AATGCTGCTTAAATTTAAAGGCTTTGATTTTACAAAGTGTGAAAGTGTTCATCAAGGAG 1864
1372 AATGCTGCTTAAATTTAAAGGCTTTGATTTTACAAAGTGTGAAAGTGTTCATCAAGGAG 2173
1373 AATGCTGCTTAAATTTAAAGGCTTTGATTTTACAAAGTGTGAAAGTGTTCATCAAGGAG 1924
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1375 AATGCTGCTTAAATTTAAAGGCTTTGATTTTACAAAGTGTGAAAGTGTTCATCAAGGAG 1984
1376 AATGCTGCTTAAATTTAAAGGCTTTGATTTTACAAAGTGTGAAAGTGTTCATCAAGGAG 2293
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1380 AATGCTGCTTAAATTTAAAGGCTTTGATTTTACAAAGTGTGAAAGTGTTCATCAAGGAG 2413
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1388 AATGCTGCTTAAATTTAAAGGCTTTGATTTTACAAAGTGTGAAAGTGTTCATCAAGGAG 2653
1389 AATGCTGCTTAAATTTAAAGGCTTTGATTTTACAAAGTGTGAAAGTGTTCATCAAGGAG 2404

Db 2654 TCGGAGTTTGTGAGAAATTTTCAAAATTAATTAATGATGATTAATTAATGATGATGAT 2713
QY 2405 TCAAAAGATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2464
Db 2714 TCAAAAGATGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 2773
QY 2465 TTAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2524
Db 2774 TTAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2633
QY 2525 AGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2584
Db 2884 AGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2893
QY 2585 GAT 2644
Db 2894 GAT 2953
QY 2645 TACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2685
Db 2954 TACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2994

RESULT 6

US-08-801-092-3
Sequence 3, Application US-08801992
Patent No. 6074850
GENERAL INFORMATION:
APPLICANT: Antelman, Douglas
APPLICANT: Gregory, Richard J.
APPLICANT: Wills, Kenneth N.
TITLE OF INVENTION: Tissue Specific Expression of
TITLE OF INVENTION: Retinoblastoma protein
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSER: TOWNSEND and TOWNSEND and CREW LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08-801-092
FILING DATE: 14-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/751,517
FILING DATE: 15-NOV-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 014930-001020
TELEPHONE: 415-576-0200
TELEFAX: 703-576-0100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2994 base pairs
TYPE: nucleic acid
STANDARDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-801-092-3

Query Match 73.8%; Score 2490.6; DH 3; Length 2994;
Best Local Similarity 93.7%; Pred. No. 0;
Matches 2688; Conservative 0; Mismatches 4; Indels 177; Gaps 1;

SEQUENCE CHARACTERISTICS:
 LENGTH: 2408 base pairs
 TYPE: NUCLEIC ACID
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 HYDROPHOBIC: NO
 ANTI-SENSE: NO
 DS: 07 708 962-1

Query Match: 2.0% Score 68.2; DB 1; Length 2408;

Best Local Similarity: 53.0%; Pred. No. 4; 5e-07;

Matches 170; Conservative 0; Mismatches 147; Indels 3; Gaps 1;

QY 1745 AGAAGCAATTGAAATCTACCTCTCTTTTCACTGTTTATAAAAGAGTATGCTAGGCT 1804
 DB 1940 AAGGCAAGAGAAATGGGCTTAAACATATTAACAGAAAGGCTATCATTTGGCA 1999
 QY 1805 AATCTGGCTAAATACATCTTTGTAAGAGCTTTGTCTGACATCCAGAAATTAATA 1864
 DB 2000 GTGACGCTTACGTCATGTAAGT---CTAAACTGGAAGTTCAATGAGTTACGAAGA 2056
 QY 1865 TCACTGACATCTTTGACACACGCTGAGAAAGAGTATGCAATCATCAGACAGGC 1924
 DB 2057 ACATAGACAGGCTTTCATTAACATTAAGTACCTGCTGCTGCTGCTGCTGCTGCT 2116
 QY 1925 ATTGACCAAAATATATATGTTGTTGATGATGATGATGATGATGATGATGATGATG 1984
 DB 2117 ATTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2176
 QY 1985 TAAATTCAAAATATATATACACATACAAAGCAATGCTGCTGCTGCTGCTGCTGCTG 2044
 DB 2177 GATTTTAAAT 2236
 QY 2045 TCAAGCTGTTTGTGATGAAA 2044
 DB 2239 AATAAGCTTTCCTGATGAAA 2256

RESULT 14

US-08-106-498A-1

Sequence 1, Application US/0810649A

Patent No. 5457049

GENERAL INFORMATION:

APPLICANT: Antonio Giordano

TITLE OF INVENTION: "TUMOR SUPPRESSOR PROTEIN PRB2"

TITLE OF INVENTION: RELATED GENE PRODUCTS, AND DNA ENCODING

TITLE OF INVENTION: THEREFOR

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Temple University of The Commonwealth

ADDRESSEE: System of Higher Education

STREET: 406 University Services Building

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19122

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08106-498A

FILING DATE: August 12, 1993

CLASSIFICATION: 445

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Mullins, J.G.

REGISTRATION NUMBER: 44,074

REFERENCE/DOCKET NUMBER: 6056-188

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-8484

TELEFAX: (215) 568-5549

TELEX: No. 5457049

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2408 base pairs

TYPE: nucleic acid

STRANDEDNESS: Single

TOPOLOGY: linear

US-08-106-498A-1

Query Match:

Best Local Similarity: 53.0%; Score 68.2; DB 1; Length 2408;

Matches 170; Conservative 0; Mismatches 148; Indels 4; Gaps 1;

QY 1745 AGAAGCAATTGAAATCTACCTCTCTTTTCACTGTTTATAAAAGAGTATGCTAGGCT 1804
 DB 2312 ATACACGACGACGACGACGCTCTTATGCTTTTCTTACAAAGGTAATATTAAGCA 2371
 QY 1805 ATCTGGCTAAATACATCTTTGTAAGAGCTTTGTCTGACATCCAGAAATTAATA 1864
 DB 2472 CTGTCGCTCTGACATCTCTGAG---CCAAATTAATAATTCAGATGAATTCAGAAA 2428
 QY 1865 TCACTGACACCTTTTGTGACACACCTGACAAAGCAATGACATGACATGACAAAG 1924
 DB 2429 AATCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2488
 QY 1925 ATTGACCAAAATATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1984
 DB 2489 AATGACGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2548
 QY 1985 TAAATTCAAAATATATATACACATACAAAGCAATGCTGCTGCTGCTGCTGCTGCT 2044
 DB 2545 AATCTGCTGACACATATATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2608
 QY 2045 TCAAGCTGTTTGTGATGAAA 2044
 DB 2609 ATAGAGTGTGTTGATGAAA 2629

RESULT 14

US-08-429-264-1

Sequence 1, Application US/08429264

Patent No. 5932440

GENERAL INFORMATION:

APPLICANT: Antonio Giordano

TITLE OF INVENTION: "TUMOR SUPPRESSOR PROTEIN

TITLE OF INVENTION: PRB2"

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Seidel, Gonda, Lavorata & Monaco, P.C.

STREET: 1800 Two Penn Center Plaza

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19102

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb

COMPUTER: IBM PS/2

OPERATING SYSTEM: MS DOS

SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08429-264

FILING DATE:

CLASSIFICATION: 540

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/106,498

FILING DATE: August 12, 1993

ATTORNEY/AGENT INFORMATION:

NAME: Monaco, D.A.

REGISTRATION NUMBER: 40,480

REFERENCE/DOCKET NUMBER: 6056-188

[illegible]

100

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OM protein nucleic search, using frame_plus_pzn model

Patent: January 18, 2003, 04:12:19 : Search time 45.4081 Seconds
(without alignments)
5391.080 Million cell updates/sec

Title: US-09-026-459A-45

Patent source: 4144
Sequence: 1 MPEKTRKTAATAAAAAAP -----TPMKPQPMNISMIFNEEV 707

Scoring table: HUSOM2

Xgapop 10.0 : Xgapop 0.5

Ygapop 10.0 : Ygapop 0.5

Equipop 6.0 : Equipop 7.0

Delopop 6.0 : Delopop 7.0

Sequences: 441 062 seqs, 15438881 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 4% summaries

Command line parameters:

Model: frame_plus_pzn model -dev xib.

Q-Zgapop 10.0 : Q-Zgapop 0.5

DB-issued Patents NA QEMT-fastop -SUFFIX-rol -MINMATCH 0.1 -LOOPEL-0

LIST 4% ISSUED PATENTS NA QEMT-FASTOP -SUFFIX-rol -MINMATCH 0.1 -LOOPEL-0

MODE LOCAL OUTPMT-PTO -NORM EXP -REAST-500 -MINLEN 0 -MAXLEN 2000000000

USER PROBAB 0.5 : USER PROBAB 0.5

WARN TIMEOUT 0 : THREAS-1 XGAPOP-10 XGAPEXT-0.5 YGAPOP-6 YGAPEXT-7

Database 1 : ISSUED PATENTS NA

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2: Zgapop 10.0 : Zgapop 0.5

3: Zgapop 10.0 : Zgapop 0.5

4: Zgapop 10.0 : Zgapop 0.5

5: Zgapop 10.0 : Zgapop 0.5

6: Zgapop 10.0 : Zgapop 0.5

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------------|
| 1 | 4068.5 | 98.2 | 2994 | 1 | US-08-294 429 2 |
| 2 | 4068.5 | 98.2 | 2994 | 4 | US-08-182 527 4 |
| 3 | 4068.5 | 98.2 | 2994 | 4 | US-08-801-092 4 |
| 4 | 4068.5 | 98.2 | 2994 | 4 | US-08-429 2 |
| 5 | 4068.5 | 98.2 | 2994 | 4 | US-08-959-639 7 |
| 6 | 4068.5 | 98.1 | 2994 | 4 | US-08-10457 1 |
| 7 | 4068.5 | 97.9 | 2994 | 4 | US-08-428 67 6A 7 |
| 8 | 4068.5 | 97.7 | 3242 | 4 | US-08-939 769 1 |
| 9 | 4068.5 | 95.7 | 3242 | 4 | US-08-539 769 1 |
| 10 | 4068.5 | 95.7 | 3242 | 4 | US-08-470-091 1 |
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| 13 | 715.5 | 17.4 | 2808 | 2 | US-08-152 721B 1 |
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| 18 | 516.5 | 12.5 | 3747 | 4 | US-09-213 294D 2 |
| 19 | 146.5 | 3.5 | 3763 | 1 | US-07-792 8059 1 |
| 20 | 136.5 | 3.4 | 4593 | 4 | US-09-404 627 3 |
| 21 | 136.5 | 3.4 | 4205 | 4 | US-09-404 627 1 |
| 22 | 133.5 | 3.2 | 10146 | 1 | US-08-353 706 2 |
| 23 | 133.5 | 3.2 | 10146 | 5 | US-08-353 706 2 |
| 24 | 133 | 3.2 | 10254 | 4 | US-08-961 527 29 |
| 25 | 131.5 | 3.2 | 6773 | 4 | US-09-166 350-27 |
| 26 | 131.5 | 3.2 | 8789 | 1 | US-08-329 264 5 |
| 27 | 131 | 3.2 | 2475 | 4 | US-09-134 0910 2 981 |
| 28 | 130.5 | 3.1 | 4883 | 1 | US-08-438 036-33 |
| 29 | 130.5 | 3.1 | 4883 | 2 | US-08-438 036-33 |
| 30 | 130.5 | 3.1 | 4884 | 4 | US-09-541 782-33 |
| 31 | 130.5 | 3.1 | 4884 | 4 | US-09-541 782-33 |
| 32 | 130 | 3.1 | 5893 | 1 | US-08-592 126-64 |
| 33 | 130 | 3.1 | 5893 | 2 | US-08-592 126-64 |
| 34 | 129.5 | 3.1 | 4868 | 1 | US-08-139 937 12 |
| 35 | 129.5 | 3.1 | 4868 | 5 | US-08-139 937 12 |
| 36 | 128 | 3.1 | 8474 | 4 | US-09-172 422 2 |
| 37 | 128 | 3.1 | 8474 | 4 | US-09-172 422 2 |
| 38 | 124 | 3.0 | 3492 | 4 | US-08-923 992A 9 |
| 39 | 123 | 3.0 | 4308 | 4 | US-09-592 054 1 |
| 40 | 122 | 2.9 | 3294 | 4 | US-08-923 992A 7 |
| 41 | 122 | 2.9 | 4743 | 4 | US-09-439 904-1 |
| 42 | 121 | 2.9 | 5461 | 4 | US-08-974-462-2 |
| 43 | 121 | 2.9 | 6152 | 4 | US-08-974-462-1 |
| 44 | 120 | 2.9 | 6008 | 1 | US-07-789 919A 5 |
| 45 | 120 | 2.9 | 6008 | 1 | US-08-005 0020 5 |

ALIGNMENTS

RESULT 1
US-08-294 429 2
Sequence 2, Application: 05/05/2004 429
Patent No. 5710255
GENERAL INFORMATION:
APPLICANT: SHEPARD, H. M.
APPLICANT: WEN, SHU F.
TITLE OF INVENTION: CHARACTERIZATION OF A N-VIRAL P11 PB
TITLE OF INVENTION: CHARACTERIZATION OF A N-VIRAL P11 PB
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: 1000 MARSHALL ST. TOWNSEND & O'NEILL LLP
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: U.S.A.
ZIP: 94111
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS DOS
SOFTWARE: Patent In Release #1.0, Version #1.40
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US-08-294 429
FILING DATE: 15 AUG 1994
CLASSIFICATION: 445
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
FILING DATE: 14 JUL 1992
NAME: RENE A. FITS
REGISTRATION NUMBER: 45,146
SUBJECT/KEYWORD NUMBER: 1990-00040005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 426 2400
TELEFAX: (415) 426 2422

1099 ATGAAAGAAATTAATGTAAGAAATGAGATGTAAGAAATGTAAGATGAT 1158
210 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 229
1099 AAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1218
210 ASATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 249
1219 AAATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1278
210 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 269
1279 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1338
210 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 289
1339 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1398
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1399 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1458
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1459 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1518
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1639 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1698
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1699 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1758
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1759 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1818
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1819 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1878
210 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 469
1879 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1938
210 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 489
1939 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1998
210 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 509
1999 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2058
210 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 529
2059 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2118
210 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 549
2119 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2178
210 TGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 569
2179 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT

2179 TGGACCCCTTCAGGACACACCTTCAGGACAAAGATATGAAATATGAGACATAGAGATTTTG 2238
570 AspcGlnIleMetMetCysSerMetTyrGlyIleValSerValIleAsnIleAspLeuAsp 589
2239 GATCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2298
590 PheTyrIleLeuValIleThrAlaTyrLysAspLeuProHisAlaValGlnIleLeuIlePheLys 609
2299 TTTCAATATCATGTAACAGATATCAAGATATCAAGATATCAAGATATCAAGATATCAAGAT 2358
610 ArgValLeuIleLysGlnIleLeuValIleValIleValIleValIleValIleValIle 629
2359 CGTGTTCATGACAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2418
630 MetGlnAlaLeuLysThrAsnIleLeuGlnIleValIleValIleValIleValIleValIle 649
2419 ATGAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2478
650 ProIleProHisIleProArgSerProTyrLysPheProSerProProLeuArgIlePro 669
2479 GCAATATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2538
670 GlyGlnAsnIleTyrIleSerProLeuLysSerProTyrLysIleSerProLeuIlePro 689
2539 GCAAGGACATCATATATTCATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2598
690 ThrProThrLysMetThrProAlaSerArgIleLeuValSerIleGlyGlnSerPheIle 709
2599 AATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2658
710 ThrSerGlnLysPheIleLysIleAsnGlnMetValIleValIleValIleValIleValIle 729
2659 ACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2718
730 ArgSerAlaGlnIleSerAsnProLysProLysProLysProLysProLysProLysProLys 749
2719 AAGAGGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2778
750 GlySerAspGlnAlaAspGlySerLysIleSerLysIleSerLysIleSerLysIleSerLys 769
2779 GGATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2838
770 LeuAlaGlnMetThrSerThrArgThrArgMetGlnLysIleLysMetAsnAspSerMet 789
2839 CTGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2898
790 AspThrSerAsnLysGlnLys 797
2899 GATAGCTCAAAACCAAGCAACACAAA 2922

RESULT 7

US-09-328-674A 7

Sequence 7, Application US/08 028673A

Patent No. 6,210,939

GENERAL INFORMATION:

APPLICANT: Gregory, Richard J.

Inventor: Daniel C.

Manaval, Kenneth

TITLE OF INVENTION: Recombinant Adenoviral Vector and

Methods of Use

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Fifth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111 4834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent in Release #1.0, Version #1.40

ADDRESSEE: Pennie & Edwards
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: U.S.A.
 ZIP: 10046-2711
 COMPUTER RELEASABLE FORM:
 MEDIUM TYPE: Floppy Disk
 OPERATOR: IBM PC compat file
 OPERATING SYSTEM: PC DOS/MS DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/048,740
 FILING DATE: 1999/04/25
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Polissant, Brian M.
 REGISTRATION NUMBER: 28,442
 REFERENCE/DOCKET NUMBER: 7499 025-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 740-0990
 TELEFAX: (212) 859-9741/0064
 TELEX: 60141 PENNIE
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 4242 base pairs
 TYPE: Nucleic Acid
 STRANDEDNESS: double
 TOPOLOGY: not relevant
 Molecule type: DNA
 33 00 008 740 2

Alignment Statistics:

Prod. No.: 0 Length: 4242
 Score: 3550/300 Matches: 687
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 85.67% Indels: 0
 Gap: 1 Gaps: 0

US 09 026 459A 45 (1-797) x US 08 048 740-2 (1-3232)

27 111 AlaValIleProGluAsnGlySerProArgThrProArgGlyGluAsnArgSerAla 130
 14 284 GTGTATAAGCAATTAATGATGATCGAACACCGAGGAGGTGCAGAACGACGTGTA 2772
 29 143 ArgIleAlaLysGlnLeuGluAsnAspThrArgIleIleGluValLeuLysLysLys 150
 16 2771 GGTAAAGCAAAACAACTAGAAAAAGATCAAGAAATTAATCAAGCTGCTGTAAGAA 2712
 29 194 GluGlyAsnIleAspGluValLysAsnValTyrPheLysAsnIleIleProPheMetAsn 170
 16 2711 GAAAGTAAATATAAGAGGTGAAAAAGTATATTTAAAAATTTTATACTTTATGAAAT 2652
 29 171 SerLeuGlyLeuValThrSerAsnGlyLeuProGluValGluAsnLeuSerLysArgTyr 190
 16 2651 TCTCTGCATTTGAAATATTAATGAGACTTCAGAGAGTTGAAATGCTTCTTAAGAGTAC 2592
 29 191 GluGlnIleTyrLeuLysAsnLysAspLeuAspAlaArgLeuPheLeuAspLys 210
 16 2601 GAAAGAAATTAAGTAAAAAAGAAATCAAGTCAAGCAATATTCTTCAATGATGATAAA 2532
 29 211 ThrLeuGlnIleAspSerIleAspSerPheGlnThrGluArgThrProArgLysSerAsn 240
 16 2541 ACTCTTCAGCTATATTCATATAGACAGTTTCAAAACAGACAGAACACAGAAAAAGTAC 2472
 29 241 LeuAspGlnIleValAsnValIleProProGlnIleThrProValArgThrValMetAsnThr 250
 16 2471 GTTATGAAGAGAGTGAAGTAAATCTCTGACAGACAGACAGTATAGGACTGTTATGAACA 2412
 29 261 PheGlnIleLeuMetMetIleLeuAsnSerAlaLeuSerAspGlnProSerGluAsnLeuIle 270
 16 2411 AGCAAAATTAATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2352

27 271 SerTyrPheAsnAsnGlySerThrValAsnProLysLeuSerIleLeuGlySerValLysAsp 290
 16 2451 TCTATATTAAACAAATGCAAGTGAATCAAAACAAAAGAGTAAATGAAAAAGATAGAAAT 2292
 29 291 TleGlyTyrIleCHeLysGlnLysPheArgLysAlaValIleGlyGlnIleTyrValGlnIle 310
 16 2291 ATAGCAATACATCTTAAAAACAAAATTCCTAAAACTGCGGACAAAGCTTCTCTCTCTCT 2232
 29 411 GlySerGlnArgTyrLysLeuGlyValArgIleGlyTyrIleArgValMetGluSerMetLeu 330
 16 2231 GCAATCAAGCAATACAAAATTCAGAGTTCCTGCAATTAACAGTAAAGTAAATTAATTA 2172
 29 341 LysSerGlnIleGluIleArgLeuSerIleGlnAsnIleSerLysLeuLeuAsnAspAsnIle 360
 16 2171 AATTCAGAAAGAAAGAAAGATTAATGATCAATCAAAATTTAAATTAATTAATTAATTAAT 2112
 29 391 PheHisMetSerLeuLeuValArgLysAlaLeuValValMetAlaIleTyrSerArgSer 410
 16 2111 TTTCATATGCTTTTATTCGCTGCTGCTTTCAGGCTTCAGGCTTCAGGCTTCAGGCTTC 2052
 29 471 ThrSerGlnAsnLeuAspSerGlyThrAspLeuSerPheProArgIleLeuAsnValLeu 490
 16 2051 ACAATCAGAAATCTGATTCGAAACAGATTCGCTTCGCTTCGCTTCGCTTCGCTTCGCT 1992
 29 491 AsnLeuLysAlaPheAspPheTyrLysValIleLeuSerPheIleLysAlaIleIleLysAsn 410
 16 1991 AATTTAAAGGCTTTGATTTTAAAGTGAATGAAAGTTTTAAATTAATTAATTAATTAATTA 1932
 29 411 LeuThrArgGluMetIleCysHisLeuGluArgCysGlnHisSerArgIleMetGluSerLeu 430
 16 1941 TTGACAGAGAGAAATGATAAACATTTAGAAATGAGCAATGCAATGCAATGCAATGCAAT 1882
 29 431 AlaTyrLeuSerAspSerProLeuPheAspLeuIleLysGlnSerLysAspArgLys 450
 16 1871 GCAAGGCTTCAGATTCAGCTTATTTGATTTTAAATTAATTAATTAATTAATTAATTAAT 1812
 29 451 ProThrAspHisLeuIleSerAlaCysProLeuAsnLeuProIleGlnAsnHisThr 470
 16 1811 GCAAGTATCAGCTTGAATGCTGCTGCTTAAATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1752
 29 471 AlaAlaAspMetTyrLeuSerProValArgSerProLysLysLysLysSerThrArg 490
 16 1751 GCAGCAATCAATGATGCTTCTCTGTAAGCAATCTCTCTCTCTCTCTCTCTCTCTCTCT 1692
 29 491 ValAsnSerThrAlaAsnAlaGlnIleThrGlnAlaThrSerAlaPheGlnThrLysPro 510
 16 1691 GTAATATCTAGTCAAAATGCAAGCAATCAAGCAATCAAGCAATCAAGCAATCAAGCAAT 1632
 29 511 LeuLysSerThrSerLeuSerLeuPheTyrLysValIleTyrArgLeuArgTyrLeuArg 530
 16 1631 TTGAAATGCTAGCTTCT 1572
 29 531 LeuAsnThrLeuCysGlnArgLeuLeuSerGlnHisSerIleLeuGlnHisSerIleLeuP 550
 16 1571 CTAAATACACTTCTGCAAGCTGCTGCTGCAAGCAATCAAGCAATCAAGCAATCAAGCAAT 1512
 29 551 ThrLeuPheGlnHisThrLeuGlnAsnGlnTyrGlnLeuMetArgAspArgLysLeuAsp 570
 16 1511 ACCCTTTCAGGACACGCTGCAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 1452
 29 571 GlnIleMetMetCysSerMetTyrGlyIleCysValIleLysAsnIleAspLeuLysPhe 590
 16 1451 CAATTAATGATGCTTCT 1392
 29 591 LysIleIleValIleThrAlaTyrLysAspLeuProHisAlaValGlnIleIleThrPheLysArg 610
 16 1391 AAAATCAATGTAACAGCAATCAAGCAATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1332
 29 611 ValLeuIleLysGlnIleGluTyrAspSerIleIleValIlePheTyrAsnSerValIlePheMet 630
 16 1331 GTTGTCAACAAAGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1272

111 AlaValIleProIleAsnGlySerProArgThrProArgArgGlyGlnAsnArgSerAla 130
112 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

RESULT 12

US-09-026-459a-1

; Sequence 1, Application US/07708962

; Patent No. 5262421

; GENERAL INFORMATION:


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16 1783  GATGGGAGAGATACACACTGATAGCTGCTTCCATGAAATCAAAATCAGGACCTCCAAAGTC 1842
17 476  LeuSerProVal -----ArgSerProLysLysCly 486
18 1843  AAGAGTCGTGATACATTAAGCTATTCATTAATTTGGTGTCTCCAAAT----- 1893
19 487  SerThrThrArgValAspSerThrAlaAsnAlaGluThrGlnAlaThrSerAlaPheGln 506
20 1894  ---CAGACCAATGCTGATTAAGTAAAGTACAAAGTACAGTACATTCACATCGCA----- 1945
21 507  ThrGluLysProLeuLysSerThrSerLeuSerLeuPheTyrLysLysValTyrArgLeu 526
22 1946  AAAAAAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1995
23 527  AlaTyrLeuArgGlnAsnThrLeuCysGluArgLeuLeuSerGluHisProGluLeuGlu 546
24 1996  PAAAGGTAGGTAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2052
25 547  HisIleIleThrThrLeuPheGlnHisThrLeuGlnAsnGluTyrGluLeuMetTyrAsp 566
26 2053  AAGACATATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2112
27 567  ArgHisLeuAspGlnIleLeuMetCysSerMetTyrGlyIleCysLysValLysAsnIle 586
28 2113  AAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2172
29 587  AspLeuLysPheLysIleIleValThrAlaTyrTyrAspLeuProHisAlaValGlnGlu 606
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33 614  ----- 614
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47 722  CysAsnSerAsp-----ArgValLeuLysArgSerAlaGluLysSerAsn 736
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49 737  ProProLys 739

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RESULT 13
US-08-152-721B-1
Sequence A: Application US-08152721B
Patent No. 5962315
GENERAL INFORMATION:
APPLICANT: Livingston, David M.
APPLICANT: Ewen, Mark E.
TITLE OF INVENTION: DNA Encoding p107 Tumor Suppressor and
Related Polypeptides
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSER: CHOATE, HALL & STEWART
STREET: 53 State Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109-2891
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08152721B
FILING DATE: 15-NOV-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pasternack Esq., Sam
REGISTRATION NUMBER: 29,576
REFERENCE/DOCKET NUMBER: 181411-011DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248 5000
TELEFAX: (617) 248-4000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2808 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: cDNA encoding p107
US-08-152-721B-1

Alignment Scores:
Prod. No.: 2,98c-51 length: 2808
Score: 715.50 Matches: 217
Percent Similarity: 39.38% Conservative: 115
Best Local Similarity: 25.74% Mismatches: 220
Query Match: 37.27% Indels: 291
DB: 2 Gaps: 23

US-09-026-459a-45 (1-797) x US-08-152-721B-1 (1-2808)
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QY 161 TyrPheLysAsnPheIleProPheMetAsnSerLeuGlyLeuValThrSerAsn 178
DB 403 GAGCATATTTTAAATGATATATTTTCAAAATCTTTTGAATAGAAATATATTAAGAGAA 462
QY 179 GlyLeuProGluValGluAsp-----LeuSerLysArgGlyGlu 191
DB 463 TGAATCTGAGATTTTCAAGTTTACTGATATATAGAAAGAGTGAATAGGATATGAA 522
QY 192 GATTTTLeuLysLysCysAspLeuAspAlaArgLeuPheLeuAspLysThr 211
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146 8454 CTCTAAGATGTACTTAATGACGCT 3477
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Search completed: January 19, 2003, 05:33:31
CPU time: 141.348 secs

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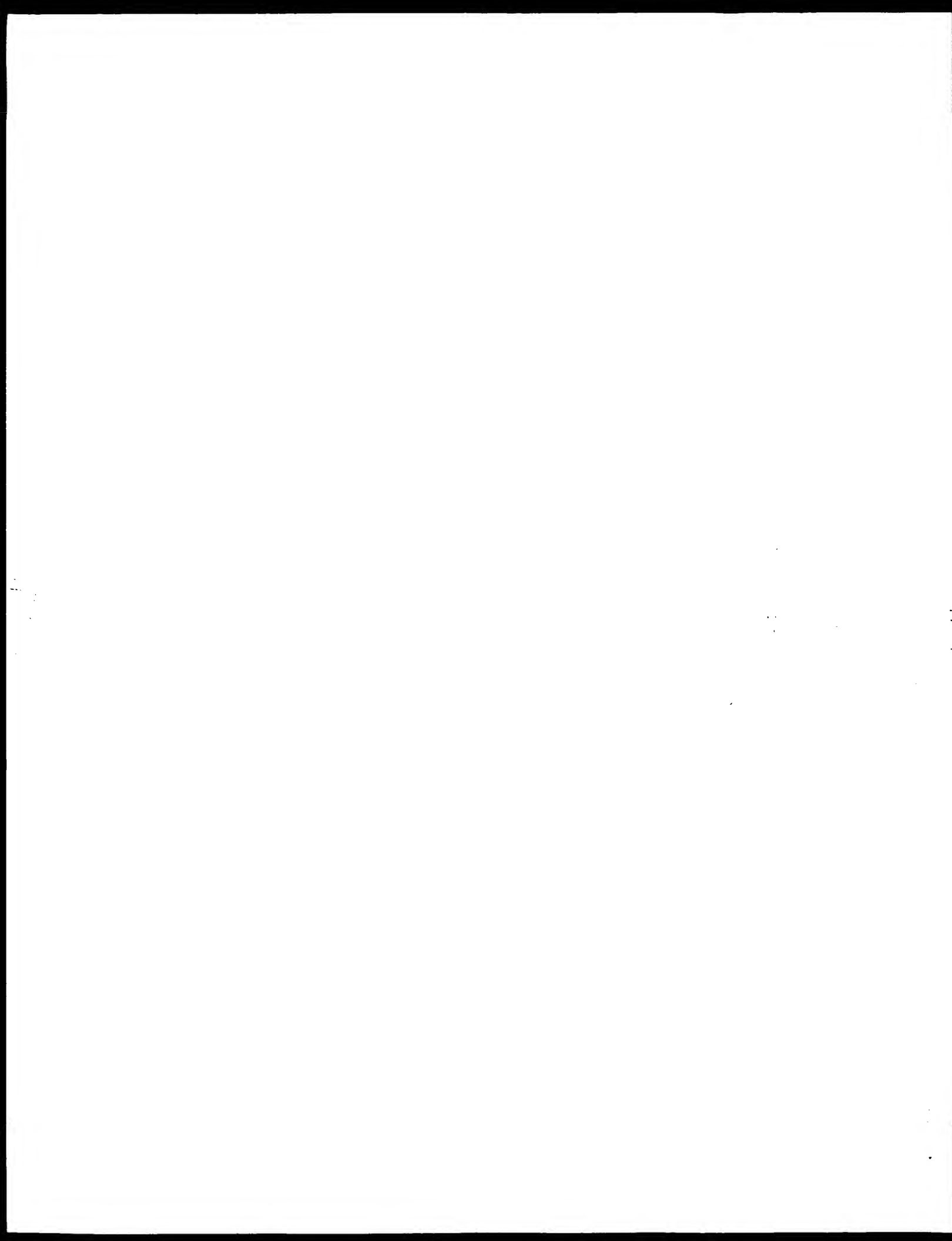
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OM nucleotide table: nucleotide search, using sw model

Run on: January 16, 2003, 15:20:22 : Search time 72.9298 Seconds
(without alignments)
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Perfect score: 3554

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Scoring table: IDENTITY_NDC

Gapop 10.0, Gapext 1.0

Searches: 441462 seqs, 153308301 residues

Total number of hits satisfying chosen parameters: 88274

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Maximum DB seq length: 2000000000

Post processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|---------------------|
| 1 | 4219.2 | 90.6 | 4242 | 1 | US-08-038-760-1 |
| 2 | 4219.2 | 90.6 | 4242 | 1 | US-08-038-760-2 |
| 3 | 4219.2 | 90.6 | 4242 | 2 | US-08-038-760-1 |
| 4 | 4219.2 | 90.6 | 4242 | 2 | US-08-038-760-2 |
| 5 | 2857.8 | 80.4 | 2994 | 1 | US-08-038-760-1 |
| 6 | 2857.8 | 80.4 | 2994 | 2 | US-08-038-760-2 |
| 7 | 2857.8 | 80.4 | 2994 | 4 | US-09-015-113-3 |
| 8 | 2857.8 | 80.4 | 2994 | 2 | US-08-038-760-1 |
| 9 | 2857.8 | 80.4 | 2994 | 2 | US-08-038-760-2 |
| 10 | 2857.8 | 80.4 | 2994 | 5 | US-08-038-760-1 |
| 11 | 2857.8 | 80.4 | 2994 | 4 | US-08-038-760-2 |
| 12 | 68.8 | 1.9 | 2808 | 1 | US-07-708-962-1 |
| 13 | 68.8 | 1.9 | 3249 | 1 | US-08-106-493A-1 |
| 14 | 68.8 | 1.9 | 3249 | 1 | US-08-106-493A-2 |
| 15 | 68.8 | 1.9 | 4853 | 2 | US-08-038-760-1 |
| 16 | 68.8 | 1.9 | 4853 | 2 | US-08-038-760-2 |
| 17 | 65.6 | 1.8 | 2808 | 2 | US-08-152-721B-1 |
| 18 | 59 | 1.7 | 7218 | 1 | US-08-232-463-14 |
| 19 | 51 | 1.4 | 3747 | 4 | US-09-213-293D-2 |
| 20 | 44.6 | 1.3 | 1803 | 4 | US-09-134-001C-799 |
| 21 | 44.6 | 1.3 | 15363 | 4 | US-08-961-527-139 |
| 22 | 44.4 | 1.2 | 29674 | 2 | US-09-641-638-651 |
| 23 | 44 | 1.2 | 19154 | 2 | US-08-487-826B-13 |
| 24 | 41.8 | 1.2 | 1056 | 4 | US-09-134-001C-1550 |
| 25 | 41.2 | 1.2 | 559 | 4 | US-09-030-607-202 |
| 26 | 41.2 | 1.2 | 559 | 4 | US-09-605-785-202 |
| 27 | 41.2 | 1.2 | 559 | 4 | US-09-439-313-202 |

| | | | | | |
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| 28 | 43.2 | 1.2 | 509 | 4 | US-09-352-514A-202 |
| 29 | 43.2 | 1.2 | 509 | 4 | US-09-352-514A-202 |
| 30 | 43 | 1.2 | 5852 | 1 | US-07-867-106-2 |
| 31 | 42.8 | 1.2 | 615 | 4 | US-08-998-416-186 |
| 32 | 42.6 | 1.2 | 1189 | 1 | US-08-307-591-2 |
| 33 | 42.6 | 1.2 | 2636 | 4 | US-09-234-827H-4 |
| 34 | 42.4 | 1.2 | 1186 | 2 | US-08-731-722-5 |
| 35 | 42.4 | 1.2 | 1775 | 1 | US-08-722-031-29 |
| 36 | 42 | 1.2 | 665 | 2 | US-08-683-795A-46 |
| 37 | 42 | 1.2 | 1864 | 4 | US-09-468-265-4 |
| 38 | 41.8 | 1.2 | 1679 | 4 | US-09-306-060-1 |
| 39 | 41.4 | 1.2 | 19124 | 2 | US-08-487-826H-13 |
| 40 | 41.2 | 1.2 | 821 | 4 | US-08-998-416-541 |
| 41 | 41.2 | 1.2 | 837 | 4 | US-08-998-416-288 |
| 42 | 41.2 | 1.2 | 2040 | 2 | US-08-705-923-7 |
| 43 | 40.8 | 1.1 | 1144 | 1 | US-08-014-944A-1 |
| 44 | 40.8 | 1.1 | 1144 | 1 | US-08-486-421-2 |
| 45 | 40.8 | 1.1 | 1144 | 1 | US-08-470-911-2 |

ALIGNMENTS

RESULT 1

US-08-038-760-1

: Sequence 1, Application US/08038760

: Patent No. 5496731

: GENERAL INFORMATION:

: APPLICANT: Xu, Houq-Ji

: APPLICANT: Renodict, William F.

: TITLE OF INVENTION: Broad-Spectrum Tumor Suppressor Genes, Gene Products and

: TITLE OF INVENTION: Methods for Tumor Suppressor Gene Therapy.

: NUMBER OF SEQUENCES: 3

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Pennic & Edmonds

: STREET: 1155 Avenue of the Americas

: CITY: New York

: STATE: New York

: COUNTRY: U.S.A.

: ZIP: 10036-2711

: COMPUTER READABLE FORM:

: MEDIUM TYPE: Floppy disk

: COMPUTER: IBM PC compatible

: OPERATING SYSTEM: PC-DOS/MS-DOS

: SOFTWARE: Patent In Release #1.0, Version #1.25

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: US/08/048,760

: FILING DATE: 1993/03/25

: CLASSIFICATION: A24

: ATTORNEY/AGENT INFORMATION:

: NAME: Fossant, Brian M

: REGISTRATION NUMBER: 28,462

: REFERENCE/DOCKET NUMBER: 7409 025 999

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (212) 790-9090

: TELEX: (212) 869-9741/8864

: TELETYPE: 66141 PENNIE

: INFORMATION FOR SEQ ID NO: 1:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 3242 base pairs

: TYPE: NUCLEIC ACID

: STRANDEDNESS: double

: TOPOLOGY: not relevant

: MOLECULE TYPE: DNA

: FEATURES:

: NAME/KEY: CDS

: LOCATION: 19..2469

: US-08-038-760-1

Query Match: 96.0%, Score: 4219.2, DB 1: Local: 4242

Best local similarity: 99.9%, Prod. No. 0:

Matches 3221, Conservative 0: Mismatches 4: Indels 0: Gaps 0:

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| 146 | 2167 | TAAAGAACTTAAATGCAATGGTAAATCATGGAGACTTGTAAATTTTAAATA | 2527 |
| 147 | 2168 | AAATGATATGGTAATTAACAGGAGGCTGGTGCAAAAAGACTGGTGAAGCAACCAAGCTT | 2610 |
| 148 | 2227 | AAATATATGATATTAATAGTAAAGATGGTGGTCAAAAAGATGGTAAGGAAGCAAGCTT | 2586 |
| 149 | 2241 | CTTAAGACATCTGAAAAAAATAGATTTTGATATTGAGGATCAGATCAAGTATGATGAATG | 2670 |
| 150 | 2287 | CTTAAGACATCTGAAAAAAATAGCTTTTGATATGAAGGATCAGATCAAGGACAGATCGAAGT | 2446 |
| 151 | 2291 | AAATATCTGGACATGATATTAATTTGACAGAAATGGGAGAAATGATTTTATTCGA | 2740 |
| 152 | 2447 | AAATATCTGGACATGATTAATTTGACAGAAATGGGAGAAATGATTTTACTCGA | 2406 |
| 153 | 2741 | ACATCAATCTGAAAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT | 2790 |
| 154 | 2807 | ACATCAATCTGAAAAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAAT | 2866 |
| 155 | 2791 | TGAGATCTGACAGATCTGATTAATTTGACAGAAATGGGAGAAATGATTTTACTCGA | 2850 |
| 156 | 2867 | TGAGATCTGACAGATCTGATTAATTTGACAGAAATGGGAGAAATGATTTTACTCGA | 2526 |
| 157 | 2951 | ATGAGATCTGATTAATTTGACAGAAATGGGAGAAATGGGAGAAATGGGAGAAATGGGAGAAAT | 2910 |
| 158 | 2527 | ATGAGATCTGATTAATTTGACAGAAATGGGAGAAATGGGAGAAATGGGAGAAATGGGAGAAAT | 2586 |
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| 160 | 2987 | TTGAGATCTGATTAATTTGACAGAAATGGGAGAAATGGGAGAAATGGGAGAAATGGGAGAAAT | 2846 |
| 161 | 2991 | TTGAGATCTGATTAATTTGACAGAAATGGGAGAAATGGGAGAAATGGGAGAAATGGGAGAAAT | 3040 |
| 162 | 2947 | TTGAGATCTGATTAATTTGACAGAAATGGGAGAAATGGGAGAAATGGGAGAAATGGGAGAAAT | 2706 |
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| 164 | 2707 | TTGAGATCTGATTAATTTGACAGAAATGGGAGAAATGGGAGAAATGGGAGAAATGGGAGAAAT | 2766 |
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| 167 | 3151 | TTGAGATCTGATTAATTTGACAGAAATGGGAGAAATGGGAGAAATGGGAGAAATGGGAGAAAT | 3210 |
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| 169 | 3211 | TTGAGATCTGATTAATTTGACAGAAATGGGAGAAATGGGAGAAATGGGAGAAATGGGAGAAAT | 3270 |
| 170 | 2987 | TTGAGATCTGATTAATTTGACAGAAATGGGAGAAATGGGAGAAATGGGAGAAATGGGAGAAAT | 2946 |
| 171 | 3271 | TTGAGATCTGATTAATTTGACAGAAATGGGAGAAATGGGAGAAATGGGAGAAATGGGAGAAAT | 3330 |
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| 173 | 3331 | TTGAGATCTGATTAATTTGACAGAAATGGGAGAAATGGGAGAAATGGGAGAAATGGGAGAAAT | 3390 |
| 174 | 3007 | TTGAGATCTGATTAATTTGACAGAAATGGGAGAAATGGGAGAAATGGGAGAAATGGGAGAAAT | 3066 |
| 175 | 3391 | TTGAGATCTGATTAATTTGACAGAAATGGGAGAAATGGGAGAAATGGGAGAAATGGGAGAAAT | 3450 |
| 176 | 3067 | TTGAGATCTGATTAATTTGACAGAAATGGGAGAAATGGGAGAAATGGGAGAAATGGGAGAAAT | 3126 |
| 177 | 3451 | TTGAGATCTGATTAATTTGACAGAAATGGGAGAAATGGGAGAAATGGGAGAAATGGGAGAAAT | 3510 |
| 178 | 3127 | TTGAGATCTGATTAATTTGACAGAAATGGGAGAAATGGGAGAAATGGGAGAAATGGGAGAAAT | 3186 |
| 179 | 3511 | TTGAGATCTGATTAATTTGACAGAAATGGGAGAAATGGGAGAAATGGGAGAAATGGGAGAAAT | 3574 |
| 180 | 3187 | TTGAGATCTGATTAATTTGACAGAAATGGGAGAAATGGGAGAAATGGGAGAAATGGGAGAAAT | 3240 |

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US-08-038-760-2/c
Sequence No. Application No. 8650760
Patent No. 5496731
GENERAL INFORMATION:
APPLICANT: XU, Hong-Ji
APPLICANT: HU, Shi-Xue
APPLICANT: Benedict, William F.
TITLE OF INVENTION: Broad-Spectrum Methods for
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036, 2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/038
FILING DATE: 1994/04/25
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Poissant, Brian M.
REGISTRATION NUMBER: 28,462
REFERENCE/BOOKET NUMBER: 7409
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PHNNE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 3232 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA
US-08-038-760-2

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Query Match: 90.6%; Score 4219.2; DB 1; Length 4242;
Best local similarity 99.9%; Pred. No. 0;
Matches 3221; Conservative 0; Mismatches 3; Indels 0; Gaps

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| QY | 331 | GAAGTAGTCATATGCTGTTCACTTTTATGAGTACAGAAAAACATAGAAATAGTGTG | 490 |
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| DB | 3230 | GACACAGATGAGAGTCGTGACATTTTATGAGTACAGAAAAACATAGAAATAGTGTG | 4171 |
| QY | 391 | CATAAATCTCTAACTATCAAAAACAAATTCATATAGATCAAAAGTCCAAATCTTAAG | 450 |
| | | | |
| DB | 3170 | CATAAATCTTAACTATCAAAAACAAATTCATATAGATCAAAAGTCCAAATCTTAAG | 4111 |
| QY | 451 | TCAAGACTGTTGAAAGATGATGATATTTGTTGACTCTTCAGCAAAATGCAAAAGCA | 510 |
| | | | |
| DB | 4110 | TCAAGACTGTTGAAAGATGATGATATTTGTTGACTCTTCAGCAAAATGCAAAAGCA | 4051 |
| QY | 511 | TGTGAACTATATATTGTGACACAAATGACAGAGTTGGATATCTTGAATAAATCTGCA | 570 |
| | | | |
| DB | 4050 | TGTGAACTATATATTGTGACACAAATGACAGAGTTGGATATCTTGAATAAATCTGCA | 2991 |
| QY | 571 | TCTGCTCAAAAGCTCTCTGGACACATATTTTATCTCAAAAGCTCAAGTATCAATG | 630 |
| | | | |
| DB | 2990 | TCCTGCTCAAAAGCTCTCTGGACACATATTTTATCTCAAAAGCTCAAGTATCAATG | 2941 |
| QY | 631 | GAAGATGATCTGTGATTTTCATTTGAGTAAATGCTAAGTGTGCTGATTTTATTAAG | 690 |
| | | | |
| DB | 2940 | GAAGATGATCTGTGATTTTCATTTGAGTAAATGCTAAGTGTGCTGATTTTATTAAG | 2871 |
| QY | 691 | CTCTCACTCCCATGTTGTGCTCAAAACCAATATAAAAGAGTGTATCACTAATATGTT | 750 |
| | | | |

2244 TAAATTAATAATCATTTAAGACAGATACAAAGATCTTCTCATGCTATTAGAGACAT 2353
2222 CAAAGCTCTTTTGAATTAAGACAGAGCTAATGATCTATTATAGTATCTATTAACCTGG 2281
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2282 TTTTCTATTAAGTAAATTAAGTAAATTAAGTAAATTAAGTAAATTAAGTAAATTAAGT 2341
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RESULT 7

US-09-315-113-3

Sequence 3, Application 09-09-015-113
Patent No. 4,799,27

GENERAL INFORMATION

APPLICANT: Antelman, Douglas
Wills, Kenneth N.TITLE OF INVENTION: Tissue Specific Expression of
Retinoblastoma Protein

NUMBER OF SEQUENCES: 46

RESPONSE ADDRESS:

ADDRESS: Townsend and Townsend and CREW LLP
STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94111

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Process #1 3, Version #1 30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US-09-315-113

FILING DATE: 19-May-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/801,092
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Ellis, Renee A.
REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 016930-001020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 703-576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2994 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-315-113-3

Query Match 80.4%; Score 2857.8; DB 4; Length 2994;
Best Local Similarity 99.9%; Pred. No. 0;

Matches 289; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 GGTTCATGCGGCTCAAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTG 61

DB 134 GGTTCATGCGGCTCAAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTG 193

QY 62 AAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTG 121

DB 194 AAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTG 253

QY 122 GGTTCATGCGGCTCAAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTG 181

DB 254 GGTTCATGCGGCTCAAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTG 313

QY 182 CATTATGTCAGAAATTAAGATACAGATCAATGTCAGATCAATGTCAGATCAATGTCAGATCAATG 241

DB 314 CATTATGTCAGAAATTAAGATACAGATCAATGTCAGATCAATGTCAGATCAATGTCAGATCAATG 373

QY 242 ACAATCTCTGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 301

DB 374 ACAATCTCTGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 433

QY 302 GGTTCATGCGGCTCAAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTG 361

DB 434 GGTTCATGCGGCTCAAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTG 493

QY 362 ACCTACAGAAATTAAGATACAGATCAATGTCAGATCAATGTCAGATCAATGTCAGATCAATG 421

DB 494 ACCTACAGAAATTAAGATACAGATCAATGTCAGATCAATGTCAGATCAATGTCAGATCAATG 553

QY 422 ATATCTCTGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 481

DB 554 ATATCTCTGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 613

QY 482 TTTTCTATTAAGTAAATTAAGTAAATTAAGTAAATTAAGTAAATTAAGTAAATTAAGTAAATTAAGT 541

DB 614 TTTTCTATTAAGTAAATTAAGTAAATTAAGTAAATTAAGTAAATTAAGTAAATTAAGTAAATTAAGT 673

QY 542 GTTTCATGCGGCTCAAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTG 601

DB 674 GTTTCATGCGGCTCAAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTGAAATCTCTG 733

QY 602 TATTCTCTGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 661

DB 734 TATTCTCTGATCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 793

QY 662 TTTTCTATTAAGTAAATTAAGTAAATTAAGTAAATTAAGTAAATTAAGTAAATTAAGTAAATTAAGT 721

DB 794 TTTTCTATTAAGTAAATTAAGTAAATTAAGTAAATTAAGTAAATTAAGTAAATTAAGTAAATTAAGT 853

